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GenCore version 5.1.6
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- protein search, using sw model M protein

August 5, 2004, 13:28:09; Search time 54 Seconds (Withbort alignmenta) 20:31.409 Million cell updates/sec

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1 MDKLDANVSSEEGFGSVEKV......ESQCHPPATSPLVAAQPSDT 402 US-10-018-257A-2 2133 erfect score: coring table: equence:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 earched:

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geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp20048;\*

Description	AAB59577 Burnan 6-4 AAB59777 Burnan 6-4 AAB59344 Furnan HTR AAB5934 Furnan HTR AAB5934 Furnan TRA AB59914 Amino 6-6 AB59914 Amino 6-6 AB59914 Amino 6-6 AB59178 Eurnan TAA AAB59178 Eurnan Furnan 6-8 AB59178 Eurnan Furnan 6-7 AB59178 Eurnan Furnan 6-7 AB59178 Eurnan Furnan 6-7 AB59178 Eurnan Furnan 6-7 AB59178 Eurnan 6-7 AB5918 Eurnan 6-7 AB59
SUMMARIES	AMBS9572 AMBS9572 AMBS9673 AMBS9673 AMBS9673 AMBS9673 AMBS9718 AMBS9718 AMBS9703 AMBS7030 AMB
DB	<b>4400000400000000000000000000000000000</b>
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Abb56347 Non-endog	Abp81807 Human dop	Adc86175 Human GPC	Abg75676 Human D1A	Add26057 Human dop		Abm04785 Rat dopam	Aar30501 N-termina	Aar21082 Dopamine	Aar30497 N-termina	Abb56350 Non-endog	Abp81808 Human dop	Aar31046 Rat D1B d	Aaw09795 D1 dopami	Aar79381 Dopamine	Aaw40802 Human D5	Aar13729 Human bet	Abg75674 Human bet	Aaw44932 Canine be	Aar13596 D1 dopami
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56	27	28	53	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

### AL I GNIMENTS

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AABS9572 standard; protein; 426 AA.
AABS9572
ID AABS
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AAB59572;

23-MAR-2001 (first entry)

Human 5-HT4(h) receptor splice variant.

Human, 5-HT4(h) receptor, 5-hydroxytryptamine; HT; serotonin; oseophageal disorder; sethma, bronchitis; pneumonia; rirtiable bowel syndrome; cancer; cytostatic; antiasthmatic; antiinflammatory; vulnerary; antisense gene therapy.

Homo sapiens.

WO200077199-A1.

14-JUN-2000; 2000WO-EP005592. 

21-DEC-2000.

99GB-00013850. 14-JUN-1999;

(JANC ) JANSSEN PHARM NV.

Jurzak M, Luyten WHML; Bender E, Pindon AN, Van Oers IP,

WPI; 2001-071270/08. N-PSDB; AAF23986.

Novel human 5-HT4 receptor splice variant useful for treating heartburn, refilms, seophagitis, Barrett esophague, esophageal cancer, achalasia, esophageal sencesis and esophageal spasss.

Claim 19; Fig 1B; 64pp; English.

(Restrictuil) receiptor protein. The protein is useful as a medicament for treating hastpure. Reflux, oseophagitis, parrett's oseophageal worder, administration oseophageal historier, administration escophageal meditary disorders, oseophageal histories, who was proteined to escophageal meditary disorders oseophageal intitation; who as then become histories of the consequence of the complete of the consequence of the complete o The present sequence is the human 5-hydroxytryptamine (HT)4(h)

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us-10-018-257a-2.rag

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Query Match

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Disclosure, Fig 1B; 64pp; English.
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22-OCT-2001, 2001US-0330457P.
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                                                                                                                           100.0%; Score 2133; DB 4;
100.0%; Pred. No. 3.6e-224;
ive 0; Mismatches 0;
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                                                                                                                                                                    Best Local Similarity 100.
Matches 402; Conservative
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          treating cancers
                                                                        Sequence 426 AA;
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ADA83841

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19-FEB-2002; 2002US-0357144P.
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(BIOM-) BIOMEDICAL CENT

Kozlov AP, Lobashev AV, Krukovskaya LL; Baranova AV, Yankovsky NK, 2003-175241/17. Determining if a nucleic acid is a marker for a phenotype/cell type of increst, by global comparison of expressed sequence tage known to be expressed in the phenotype/cell type with all ESTs expressed in normal

# Claim 29; Page 243-244; 516pp; English.

The invention relates to a novel method for determining if a mustice from a marker for a predetermined phenotype/cell type of interest from this old agreement of a group of expressed esquence takes its predetermined phenotype/cell type of interest with all SES septement all the phenotype/cell type of interest with all SES septement of the phenotype/cell of interest. A mathod of the invention is useful for the phenotype cell type of interest from a biological species that are preferentially expressed in the phenotype or cell type of interest from a biological species. Preferably chenotype or cell type of interest from a biological species, byte of interest from a biological containing with a strength of a streaming the procession of colon of the invention as a shouseful for determining the procession of colon cancer in a human, for detecting a tumour cell, and for regulating or the invention is the species or high salt ordeful of a tumour cell, and subject of the invention is the predeting a tumour cell, and subject of the invention is useful or determining when the predeting a tumour cell, and for regulating or tumour sell, and the predeting as an immunogen for vegatiating an animal. The present of sequence of the invention is user a sequence of the present of a subject of the invention is user animal mining of the invention is used. tumour-associated antigen of the invention.

# Sequence 388 AA;

0; Indels 14; Gaps 95.7%; Score 2042; DB 6; Length 388; 96.5%; Pred. No. 2.9e-214; ive 0; Mismatches 0; Indels 14 Query Match
Best Local Similarity 96.5'
Matches 388; Conservative

STITINGSTHVLRDAVECGGØMESQCHPPAISPLVAAQPSDT 402 STTTINGSTHVLRDAVECGGGWESQCHPPATSPLVAAQPSDT 388 361

DA83841

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human; marker; expressed sequence tag; BST, arabidopsis; tumour;
stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krukovskaya LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV,
standard, protein, 388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2001; 2001US-0293999P.
22-OCT-2001; 2001US-0330457P.
19-PEB-2002; 2002US-0357144P.
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                                                                                                                 20-NOV-2003 (first entry)
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                                                                                                                                                                       Human HTR45 protein
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                          ADA83841;
                                                                                                                                                                                                                                                                                            vaccine.
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Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tage known to be expressed in the phenotype/cell type with all 557s expressed in normal

WPI; 2003-175241/17.

N-PSDB; ADA83839

Claim 29; Page 241-243; 516pp; English.

The invention relates to a nowell method for determining if a nutriest coild may a market to a nowell method for determining if a nutriest coild may a nutriest of a group of expressed termining when the section The method comprises participating a global comparison to fa group of expressed interest the method comprises participating a global comparison of a group of expressed interest with all ISSTs expressed in the phenotype/cell type of interest with all ISSTs expressed in the phenotype/cell of interest. A method of the invention is useful for phenotype/cell of interest. A method of the invention is useful for phenotype or cell type of interest from a loidogistal species, preferably phenotype or cell type of interest from a loidogistal species, therefore as a numer cell, and the preference of preference of

## Sequence 388 AA;

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61 SLAFADLLVSVLVMPPGAIELVQDIWIYGEVFCIVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                        61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                  9
                                                                                                         1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
95.7%; Score 2042; DB 6; Length 388; 96.5%; Pred, No. 2.9e-214;
                                          Indels
                                          0; Mismatches
                   96.54;
                       Best Local Siminary,
Matches 388, Conservative
   Ouery Match
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셤 È a 121 ALCCOPLVYRNKATPLRIALALGGCWVIPTFISFLPIMCGWNNIGIIDLERSLNGGLGGD 180

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120
                                                                         61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                 AICCOPLVYRNKWTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; trace amine receptor; TAS receptor; G protein-coupled receptor; GFCF; chronsome 6, hematological disorder; CMS disorder; asthma; enteriorist obstructive pulmonary disease; COPD; cardiovascular disorder; gastrointestinal disorder; cancer; diabetes; obesity;
                                                                                                                                                                                                                                                                                            MDKLDANVSSEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                           MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                         SLAFADLLVSVLVMPFGAIELVQDIWIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                    OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCI IMGCFCLCWAPFFVTNIVDPPID
                                                                                                                                                                                                                                                         QMLQRAGASSESRPQSADQHSTHRWRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide encoding a G protein-coupled receptor polypetide useful for treating diseases, e.g. hematological, cardioascular, agastrontestinal or genitourinary disorders, asthma, cancer, diahetes, gastrontestimal or genitourinary disorders, asthma, cancer, diahetes,
                                                                                                                                 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                  ---IEKRKRNQNSNSTYCVFMVNKPYAITCSVVAPYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a protein 31% identical to human TAS receptor.
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17-APR-2002, 2002US-0372809P.
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                                                                                                     QMLQRAGASSESRPQSADQHSTHRMRIETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFID 300
                                                                                                                                                             The present invention provides the protein and coding sequences of buman TAA receptor, which is a d-protein coupled receptor. The sequences are useful in the treatment of hematological disorders, chronic obstructive pulmonary disorders, earlier an introvise system (USB) disorders, disheren observe, cancer and genito-infavor disorders, disheren observe, as a probe protein used to determine the expression levels of the human "4 receptor protein used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Himman, G-protein coupled receptor; TWA receptor; receptor; cytostatic, heemostatic, anticathmatic, cardiant; antidiabetic; anorectic; asthma meuroprotectic; anticherbhatic; cardiant; antidiabetic; anorectic; asthma meuroprotectic, heemostopical disperse; ORS disorder; CORS, cardianty disorder, CORS (GROCER; probe 12); cancer; gentle-unimary disorder; probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polymucleoride encoding G-protein coupled receptor, TA4 receptor, useful for treating hematological disorders, asthma, cardiovascular disorders, disorders, obesity, cancer and genito-utinary disorders.
                                                                                                                     OMI.QRAGASSESRPQSADQHSTHRMRTETKAAKTLCI IMGCPCLCWAPPPVTNIVDPPID
PHAI EKRKFNONSNSTYCVFWVNKPYAI TCSVVAFYI PFLLMVLAYYRI YVTAKEHAHOI
                                                            ---IEKRKFUQNSNSTYCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAXEHAHQI
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                                                                                                                                                                                                                         Human TA4 receptor expression assay probe protein.
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Pred. No. 2.9e-214;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                              AA019909 standard; protein; 388
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15-NOV-2001; 2001US-0331393P.
17-APR-2002; 2002US-0372811P.
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Best Local Similarity 96.5%;
Matches 388; Conservative (
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us-10-018-257a-2.rag

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modulating the activity of the GPV in a disease, e.g., memerationical disorders, a CNS disorder, chronic obstructive pulmonary disease (COPD) asthma, a cardiovascular disorder, a gastrointestinal disorder, cancer, dishes, obserty or genitourinary disorder.
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Gaps
                                              14;
                         Length 388;
                                                0, Indels
                     Score 2042; DB 6;
Pred. No. 2.9e-214;
0; Mismatches 0;
                     95.7%;
                                Best Local Similarity 96.5
Matches 388; Conservative
Sequence 388 AA;
                       Query Match
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SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 AICCOPLUYRNKWIPLRIALMIGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180 YTVPCQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRPSILGCTVPC 360 OMLORAGASSESRPOSADQHSTHRMRTBTXAAXTLCIIMGCFCLCWAPFFVTNIVDPFID 300 9 1 MDKLDANVSSEBGFGSVEKVVLLTFLSTVIIMAILGNLLVMVAVCWDRQLRKIKTNYPIV AICCOPLYKRIKATPLRIALMLGGCWVIPTFISFLPIMGGWNNIGIIDL------OMLORAGASSESRPQSADQHSTHRWRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID YTVPCQVWTAPLWLGYINSGLNPFLYAFLNKSFRRFFLIILCCDDERYRRPSILGGTVPC 1 MDKLDANVSSEBGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 181 FHAIEKRKFNQNSNSTYCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYRIYVTAKEHAHQI STITINGSTHVLRDAVECGGOWESOCHPPAISPLVAAQPSDI 402 7 61 121 170 241 227 301 287 361

STITINGSTHVLRDAVECGGOWESOCHPPATSPLVAAOPSDI 388

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ABP81768 standard; protein; 388

(first entry 04-MAR-2003 ABP81768;

Human 5-HT4 receptor protein SEQ ID NO:18.

of proceal-coupled recoptor GGCR anticent popule, gene tharpy, of proceal-coupled recoptor GGCR anticents of individual contents of processor, and the contents of growth-related disease, cal respectation related disease, AIDS cancer, limmological-related contents of profitering disease, AIDS cancer, AIDARDO OGICAL-related contents of profitering for a content of sease and anticent of sease, and the processor of sease and the contents of sease and the conte

hypertension, hypotension, renal disorder, rheumatoid arthritis, trauma, ulcer.

Homo sapiens.

WO200261087-A2.

08-AUG-2002

19-DEC-2001, 2001WO-US050107.

(LIFE-) LIFESPAN BIOSCIENCES INC.

Brown JP; Roush CL,

WPI; 2003-046718/04. N-PSDB, ABZ42612 New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for tiagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure, Fig 1; 523pp, English.

The present invention describes setting to apprictes (1) comprising: (a) according to the control of a partial of a partial of a setting to the control of a set e setting to the control of a setting to the control of a set e setting to the control of a set e setting to the control of a set e setting to the control of a setting to the present of the present of a setting to the present of the present of a setting to the present of a set

Sequence 388 AA;

9 1 MDKLDANVSSEBGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 95.7%; Score 2042; DB 6; Length 388; 96.5%; Pred, No. 2.9e-214; 0; Indela 0; Mismatches Best Local Similarity 96.5 Matches 388; Conservative Query Match

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SLAFADLIVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 SLAFADLLVSVLVWPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 9 MDKLDANVSSEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 61

AICCOPLYRNKMTPLRIALMIGGCWYIPTFISFLPIMOGWNNIGIIDLERSLNOGLGOD 180 121 AICCOPLVYRNKMTPLRIALMIAGGCWVIPTFISFLPIMGGMNNIGIIDL------ 169 FHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI 181 ઠ 셤 ò

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226

66/1/1/9 5 15:13:08 2004 Thu Aug

ABB56323 standard; protein; 388 AA. (first entry) 18-FEB-2002 ABB56323: RESULT 8 ABB56323 

Human, G protein-coupled receptor, GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.

Non-endogenous human GPCR protein, SEQ ID NO: 439

Homo sapiens.

Synthetic.

WO200177172-A2.

18-OCT-2001

05-APR-2001; 2001WO-US011098

D7-APR-2000; 2000US-0195747P.

(AREN-) ARENA PHARM INC.

Liaw CW, Lehmann-Bruinsma K,

Lin I,

WPI; 2001-648759/74 N-PSDB, ABI97959. Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions of GPCRs.

Claim 1; Page 240-242; 394pp; English.

The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of consider compounds as reseptor againsts, inverse againsts to partial againsts. Such againsts as the sequence of partial againsts, disorders associated with GPCRs. The present sequence is a non-endogenous vession of a known human GPCR.

Sequence 388 AA;

Gaps 1; Indels 14; 95.5%; Score 2037; DB 4; Length 388; 96.3%; Pred. No. 1e-213; tive 0; Mismatches 1; Indels 1v Conservative Local Similarity Best Local Sim: Matches 387; Query Match

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AICCOPLYTRICATPLEIALMIGGGRAVIPTFISFLPIMOGMNNIGIIDLERSLNOGIGOD 180 181 FHAIBKRKFNQNSNSTYCVFMVNKPYAIICSVVAFYIPFILMVLAYYRIYVTAKEHAHQI 240 AICCQPLVYRNXOTPLRIALMIGGCWVIPTFISFLPIMQGWNNIGIIDL------121

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170 ---IBKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIXVTAKEHAHQI 226

301 YTVPGQVWTAFLWIGYINSGLNPFLYAFILNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360

5-HT4 serotonin receptor; 5-HT4R; 5-HT4A; adenylate cyclase; agonist; Serotonin receptor encoded by full-length human serotonin 510 clone. 402 STTTINGSTHVLRDAVECGGGWESGCHPPATSPLVAAQPSDT Ź AAR57032 standard; protein; 388 (first entry) (revised) 25-MAR-2003 04-MAR-1995 S10 clone. 287 361 347 AAR57032, AAR57032 RESULT 음 Š 셤 \*\*\*\*

W09414957-A2. Homo sapiens

07-JUL-1994

93WO-US012586 22-DEC-1993; 92US-00996772

24-DEC-1992;

(SYNA-) SYNAPTIC PHARM CORP.

Weinshank RL; Branchek TA, Gerald C, Hartig P,

WPI; 1994-234695/28. N-PSDB; AA068831,

Memalian FIFT serrorian receptor, correge DNA, probes, anti-tense olden mulcipul and antibodise - useful for treating continuous abnormal 5-14T acceptor expression, for screening for (ant) agonises, prodn. of transgenic animals etc. 

Example; Page 96-98; 161pp; English.

S10 is a 270 Mp Engement identified when act brain CDMN uses used as template in a PCP with the desperance primers 1.17 (AMG6883) and 5.5 (AMG6883). The clone trepresents a poperhially two sercotomic receptor. By direct PCR snailysis of bacterial pools, sib selection and filter whybridisation, two full-inaph CDMN clones '150.0'8', 5.5Mp' and S10-55, 4.5Mp' were determined, The full length human S10 clones are given in AMG68831 and AMR70732. Begs Il describes these asculones as clone S10-55 and poperhise them as clone S10-55. correct PN field.)

Sequence 388 AA;

14; Gaps Query Watch
Best Local Similarity 95.0%; Pred. No. 3.30-31, Length 388;
Matches 382; Conservative 3; Mismatches 3; Indels 1.

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1 MDKLDANVSSEEGFGSVEKVVLLIPLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV MDKLDANVSSEGFGSVEKVVLLTPLSTVILMAILGNLLVWVAVCWDTQLRKIKTNYFIV

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SLAPAHLLYSVLVMPFGAIELVQDIWIYGQLFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY

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241 301 361 347

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300 240 226 286 360

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287 YTVPGQLWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLILLCCDDERYRRFSILLGQTVPC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated DNA molecule according ammallan t-FIFT receptor is cultated, having the exquence HRN-Y-X-COOM wherein Y is Dp 101-1177 of AAGG822 and X is Dps 117-1251 of AAGG822 and S. Land a 270 D Dp fragment identified when rat brain cDNA was used as template in a 270 D Dp fragment identified when rat brain cDNA was used as template in a PCR with the degenerate primers 31 TO HAAGG8323 and 5. LAAGG8323 in factived from well connerved regions among several serectonia receptors in the 31d and 54D putative transmembrane domains a The peptide sequence correspond to the close correspond to a transmembrane YV-like domain and the close expressing a posentially two serectorian receptors by direct PCR analysis as of bacteria pools is beleation and titter hybridisation, two
                                  SLAFADLLVSVLVMPFGAIELVQDI#VYGEMPCLVRTSLDVLLTTASIFHLCCISLDRYY
       SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                    121 AICCOPLVYRNIONTPLRIALMIGGCWVIPTRISFLPIMOGWNNIGIIDLERSLNOGIGOD
                                                                                                                                                                                                                                                                                                     QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                                                                                                                                                                                                227 QVLQRAGAPAEGRPQPADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                                                                                                                                                                                                                                                  YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLILLCCDDERYRRPSILGQTVPC
                                                                                                                                   121 AICCOPLVYRNKOTPLRIALMLGGCWVIPWFISFLPIMGGWNNIGIVDL-----
                                                                                                                                                                                                     181 FHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOI
                                                                                                                                                                                                                                                   ---IEKRKFNONSNSTYCVFMVNKPYALTCSVVAFYIPFLLMVLAYYRIYVTAKEHARQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-HT4 serotonin receptor; 5-HT4R; 5-HT4A; adenylate cyclase; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neumalian FIFH serotonin receptor, corresponding the sense of intolving abormal 5-17H serotonin receptor approach for treating conditions intolving abormal 5-17H seeptor expression, for screening for (ant) agosists, proch. of transgenic animals etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTTINGSTHVLRDIVECGGGWESOCHPAASSPLVAAOPIDT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STTTINGSTHVLRDAVECGGQWESQCHPPATSPLVAAQPSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weinshank RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat 5-HT4 receptor encoded by S10-95 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 88-91; 161pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR57030 standard; protein; 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-00996772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-234695/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ57030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 YIVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC 346
                                                                                                QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFID 300
                                                                                                                                           OMIORAGASSESRPOSADQHSTHRMRIETKAANTLCIIMGCFCLCWAPFFVTNIVDPFID 286
                                                                                                                                                                                             YTVPGOVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDKLDANVSSEEGFGSVEKVVILIFLSTVILMAILGNILVMVAVCWDRQLRKIKTNYFIV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor; TAA receptor; receptor; cytostatic; hammonseatic; antiasthmat; natidathmat; antidathmat; antiasthmat; sethma; neuroprotective, hammatological disorder; COPP; cardiovascular disease; CNS disorder; diabetes; obesity; cancer; genito-urinary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of human TAA receptor, which is a 6-protein coupled receptor. The sequences are useful in the treatment of hemstological disorders, carbon to obstructive pulmonary disease, sethma, cardiovascular disorders, central nervotive system (CMS) disorders, disbates, obstructive system (CMS) disorders, disbates, obstructive disorders. The present sequence is the protein swismaw/070528/584_GANYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         weal polymucleotide encoding G-protein coupled receptor, TAM receptor, useful for treating hemetological disorders, estims, cardiovascular disorders, diaberes, Obesity, cancer and genito-utinary disorders.
FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                              170 ---IEKRKFNONSNSTYCVFMVNKPYALTCSVVAFYIPFLLIVLAYYRIYVTAKEHAHOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TA4 receptor associated protein swissnew/070528/5H4_CAVPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAO19905 standard; protein; 388
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15-NOV-2001; 2001US-0331393P.
17-APR-2002; 2002US-0372811P.
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370; Conservative
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402002101043-A2.

Homo sapiens

11-AUG-2003

AA019905;

A019905

06-JUN-2002;

19-DEC-2002

WPI; 2003-148806/14. (FARB ) BAYER AG

Zhu Z;

MDKLDANVSSKEGFGSVEKVVLLTFLSAVILMAILGNLLVAVAVCRDRQLRKIKTNYFIV 60

Sequence 388 AA;

Query Match Local

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AICCOPLVYRNKWTPLRIALMLGGCWVIPTFISPLPIMOGWNNIGIIDLERSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286
Splice variants of human 5-HT4 receptor - and corresponding DNA, vectors, antibodies, etc.
                                                                                     This sequence represents the amino acid sequence for the human serocomin receptor pal/cevariant 5-HT4(d) 3-HT4(d) 3-M2471451) irreceptor pal/ceptides can be used to screen for substances, especially ligands, useful in the treatment of GTM disorders associated with abnormal 5-HT4(d) receptor expression or gastrointestinal disorders associated with disperse of the disorders associated with abnormal 5-HT4(d) receptor expression or gastrointestinal disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLAFADLLVSVLVMPFGAIBLVQDIWIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMLQRAGASSESRPQSADQHSTHRMRTETRAAKTLCIIMGCFCLCWAPPFVTNIVDPPID
                                                                                                                                                                                                                                                                                                          1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
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                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                         *Match B8.0%; Score 1878; DB 2; Local Similarity 96.2%; Pred. No. 2.3e-196; R8 359; Conservative 0; Mismatches 0;
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                                                           Claim 1; Page 44-45; 58pp; Prench
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                                                                                                                                                                                                               Sequence 360 AA;
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                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                   Best Loca
Matches
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                                                                                                                                                                                                                                                                                61 SLAPADLLUSVLVMPPGALELVQDIWIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                                                                                                                       SLAFADLLVSVLVNAFGAIBLVQDIWFYGEMFCLVRTSLDVLLTASIFHLCCLSLDRYY 120
                                                                                                                                                                                                                                                                                                                                                AICCOPLYRNKMTPLRIALMIGGGWVIPTFISFLPIMOGMNNIGIIDLERSINGGLGOD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
          full-length cDNA clones (810-87, 5.5kb; and 810-95, 4.5kb) were determined. The peptide sequences are only 96.7 identical diverging in the second half of the C-terminal tails, domesteem of poem. 353. The entire 3' unitramisted elegions are totally divergent. (Dpdated on 25-908-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMLORAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                    Human, serotonin receptor, splice variant, alternative splicing; 5-HT4;
serening, ligand, central nervous system; CNS; disorder; expression;
gastrointestinal disorder.
                                                                                                                                                                                                                                                                                                                                                                   ---IEKRKFNHNSNSTFCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMLQRAGATSESRPQTADQHSTHRWRTETKAAKTLCVIMGCFCFCWAPFFVTNIVDPPID
                                                                                                                                                                                                                 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                 181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFILMVLAYYRIYVTAKEHAHQI
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                                                                                                                                                 Length 406;
                                                                                                                                                                                17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTTINGSTHVLRDAVECGGOWESQCHPPATSPLVAAQP 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human serotonin receptor splice variant 5-HT-4(d).
                                                                                                                                                 88.1%; Score 1879; DB 2;
89.0%; Pred. No. 2.1e-196;
iive 13; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY14522 standard; protein; 360 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97FR-00015037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97FR-00015037
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                                                                                                                                                                                     Matches 355; Conservative
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                                                                                                                                                                   Similarity
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                                                                                                                    Sequence 406 AA;
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Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMLORAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGOTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 YIVPGQVWIAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC 346
                                                                                                                                                                                                                                                                                                                                       The invention relates to d protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor againsts, inverse againsts or partial againsts. Such againsts are useful as the therapout against or before a some of a some of a some endogenous version of a known human GPCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDKLDANVSSEGFGSVEKVYLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDXLDANVSSEEGFGSVEKTVLLTFLSTVILMAILGNLLVMVAVCWDRQLRXIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLAFADLLVSVLVMPFGAIELVODIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AICCOPLVYRNKMTPLRIAIALGGGWVIPTFISFLPIMQGWNNIGIIDL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1874; DB 4;
Pred. No. 6.9e-196
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                  Claim 1, Page 240; 394pp; English
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      05-APR-2001; 2001WO-US011098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.9%;
                                              07-APR-2000; 2000US-0195747P
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Matches 359; Conservative
                                                                                   (AREN-) ARENA PHARM INC
                                                                                                                        Lehmann-Bruinsma K,
                                                                                                                                                             WPI; 2001-648759/74
                                                                                                                                                                                   N-PSDB; ABI97958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 387 AA;
                                                                                                                                                                                                                                                             of GPCRs.
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                                                                                                                                                                                                            This sequence represents the amino acid sequence for the human serotonin receptor splice variant 5-HTV(6). The 5-HTV(6) and 5-HTV(6) MAX1452) receptor polypeptides can be used to screen for substances, especially ligands, useful in the treatment of CNR disorders associated with abnormal 5-HTV(6) receptor expression or gastrointestinal disorders associated with abnormal 5-HTV(6) receptor expression or gastrointestinal disorders
                                                                                                                        vectors,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AICCQPLVTRNKMTPLRIALMLGGCWVIPTFISPLPIMQGWNNIGIIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMLORAGASSESRPQSADQHSTHRMRTETKAAKTICTIMGCFCLCWAPFFVTNIVDFFID
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      ö
   Gastineau M, Blondel
                                                                                                                  Splice variants of human 5-HT4 receptor - and corresponding DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 1877; DB 2,
Pred. No. 3.2e-196;
0, Mismatches 4;
   Dahmoune Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
                                                                                                                                                                       Claim 1; Page 41-42; 58pp; French.
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Fischmeister R, Langlois M,
Hoebeke J;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2%;
Matches 359; Conservative
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                                                          WPI; 1999-349539/30
                                                                                N-PSDB; AAX79306
                                                                                                                                                                                                                                                                                                                                                          Sequence 380 AA;
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181 FHAIBKRAKTNONSNSTYCVEMANKEYA.TTCSVNAFTIPFILAWILAYTRIVTAKEEHHOI 240
170 ---ERCHANGASSTYCVEWANKEYA.TTCSVVAFYIPFILAWILAYTRIVTAKEEHHOI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 YTVPGQWTAFLMLGYINGGLNPFLYAFLAKSFRAPLIILCCDDERYRRPSILGGTVC 360
287 YTVPGQWTAFLMLGYINGGLAPELYFRANSFRRAPLIILCCDDERYRRPSILGGTVFC 346
YTVPGQWTAFLMLGYINGGLAPELYFRANSFRRAPLIILCCDDERYRRPSILGGTVFC 346
                                                                                                                                                                                                                                                                                                                     identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SIAFADILVSVLVMPFGAIELVQDIMIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 QMLQRAGASSESRPQSADQHSTHRMRTETKAKKTLCIIMGCFCLCWAPFFVTNIVDPPID 286
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to of protein-coupled respectors (RCFMs) for which the endogenous ligand has been identified. Mon-endogenous constitutively activated versions of known Opers are used in the invention for the direct identification of condidate compounds as receptor agonities. Inverse equities or partial agonities. Such agonises are useful as the represented agonities are useful as presented agonities are useful as presented agonities are useful as presented agonities are useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%; Score 1873; DB 4; Length 360;
96.0%; Pred. No. 8e-196;
tive 0; Mismatches 1; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, Page 244-245; 394pp; English.
                                                                                                                                                                                                                                    Lin I;
                                                                                                                                                                                                                                    Liaw CW,
                                                                                                                           05-APR-2001; 2001WO-US011098
                                                                                                                                                          07-APR-2000; 2000US-0195747P
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Best Local Similarity 96.0
Matches 358; Conservative
                                                                                                                                                                                               (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                      WPI; 2001-648759/74.
N-PSDB; ABI97961.
                                                                                                                                                                                                                                    Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 360 AA;
                                                     WO200177172-A2
Homo sapiens.
Synthetic.
                                                                                       18-OCT-2001
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UG-10-018-257A-2 2133 2138 URCLDANVSSEEGFGSVEKV......ESQCHPPATSPLVAAOPSDT 402 itle: erfect score: equence:

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389414 seqs, 51625971 residues earched:

389414 otal number of hits satisfying chosen parameters:

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| 1. (cgf) 2 ()prodata/2/isa/sB. cgf. psp: |
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| 1. (cgf) 5 ()prodata/2/isa/sB. cgf. psp: |
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| 1. (cgf) 7 ()prodata/2/isa/sB. cgf. psp: |
| 1. (cgf) 8 ()prodata/2/isa/sB. cgf.

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the acore of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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esult		Query					
No.	Score	Match	Length DB	图	ID	Description	
1	2042	95.7	388	н	US-08-446-822-8	Sequence 8, Appli	-11
61	2042	95.7	388	4	US-09-328-314-8	Sequence 8, Appli	٠.
m	2042	95.7	388	'n	PCT-US93-12586-8	Sequence 8, Appli	
4	1886	88.4	406	4	US-09-328-314-4	4	4
ß	1884	88.3	406	Н	US-07-996-772A-4	4	٠,
φ	1884	88.3	406	Н	US-08-446-822-4	Sequence 4, Appli	٠.
7	1884	88.3	406	ß	PCT-US93-12586-4	4	٠,
œ	1878	98.0	360	4	US-09-555-313B-4	4	·H
6	1877	88.0	380	4	US-09-555-313B-24	Sequence 24, Appl	_
10	1877	98.0	760	4	US-09-555-313B-2	~	٠.
11	1769	82.9	387	н	US-07-996-772A-2	~	•н
12	1769	82.9	387	٦	US-08-446-822-2	Sequence 2, Appli	44
13	1769	82.9	387	4	US-09-328-314-2	~	٠,
14	1769	82.9	387	S	PCT-US93-12586-2	7	~
15	1239	58.1	261	Н	US-08-446-822-15	15,	~
16	1239	58.1	261	4	US-09-328-314-15	15	н
17	1239	58.1	261	ß	PCT-US93-12586-15	15,	ч
18	939	44.0	178	н	US-07-996-772A-6	Sequence 6, Appli	•н
19	939	44.0	178	-	US-08-446-822-6	6,	••
20	939	44.0	178	4	US-09-328-314-6	9	4
21	939	44.0	178	ß	PCT-US93-12586-6	Sequence 6, Appli	
. 22	582.5	27.3	446	Н	US-07-626-618A-21	21,	н
23	582.5	27.3	446	-	US-08-333-977-21	21,	_
54	580.5	27.2	446	7	US-07-969-267B-4	4,	-
52	580.5	27.2	446	4	US-09-168-510-4	Sequence 4, Appli	
56	569	26.7	483	Н	US-08-194-338-7	7	н
27	266	26.5	418	m	US-08-817-869-12	Sequence 12, Appl	_

1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAII,GNLLVMVAVCWDRQLRKIKTNYFIV 60 1 MDXLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIXTNYFIV

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Sequence 2, Appli	Sequence 22, Appl	Sequence 22, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 17, Appl	Sequence 8, Appli	Sequence 9, Appli	Sequence 5, Appli	Sequence 12, Appl	Sequence 12, Appl
PCT-US91-00909-2	US-07-626-618A-22	US-08-333-977-22	US-07-969-267B-2	US-09-168-510-2	US-07-686-591-4	US-07-970-715-4	US-08-444-734A-2	US-07-791-936A-2	US-08-383-781B-2	US-08-748-485-6	PCT-US91-00909-4	US-08-087-772A-17	US-08-194-338-8	US-08-467-559B-9	US-08-444-734A-5	US-08-467-568-12	US-09-030-582-12
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417	446	446	477	477	475	475	487	477	477	358	413	413	417	365	413	413	413
26.5	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.3	26,3	26.2	25.8	25.8	25.8	25.7	25.6	25.6	25.6
5.595	563.5	563:5	563.5	563.5	562.5	562.5	562.5	561.5	561,5	559	550	549.5	549.5	549	547	547	547
28	. 29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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US/08446822 PRARMACBUTICAL CORPORATION NAN ENCODING 5-HT4 SEROTONIN RECEPTORS AND USES THEREOF 15: 5: 6: 6: DUNMAN LLER PLAZA LLER PLAZA  N:	Length 388, Indels 1
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287 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 346
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287 YTVPSTAFFALGYISSGLNPFLAFARSFRAFLTILCCDERYRRPFLAGYTVPC 346
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                                                                                                                                  361 STTTINGSTHVLRDAVECGGGWESQCHPPATSPLVAAQPSDT 402
                                                                                                                                                                                  347 STTTINGSTHVLRDAVECGGOWESOCHPPATSPLVAAOPSDT 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Rattus norvegicus
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61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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Beat Local Smilarity 89.2% Pred. No. 2.78-143,
Matches 356; Conservative 13; Wismatches 16; Indels 14; Gaps
APPLICANT: Gerald, Christophe
APPLICANT: Grandle, Christophe
APPLICANT: Brandle, Theresa A.
APPLICANT: Brandle, Theresa A.
APPLICANT: Brandle, Theresa A.
TITLE OF INVENTION IN RECEDING 5-HT4A SEROTOMIN
TITLE OF INVENTION: REPROSE AND USES THEREOF
ANDRESSES. COOPER S.
ADDRESSES: COOPER S.
CITT: NEW YORK
CITT: NEW YORK
ZIP: 10112
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TELEPHONE 1217 664 9550
TELEPHONE 1217 1664 9550
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INDEMARY 12253 0000 IN TELEX 42253 000 IN TELEX 42253 000 IN TELEX 1217 464 9550
SEQUENCE CHARACTERISTICS
INDEMARTINE 406 SEMIDO acide
TIPE: amino acide
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/996,772A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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RESULT 6 US-08-446-822-4

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241 OMLGRAGASSESRPQSADQHSTHRWRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
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                                                  APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-H14 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Parentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12586
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               TITLE OF INVESTIGATION. MAD BECODING.
TITLE OF INVESTIGATION. AND USES THEN
HUMBER OF SECURICIS. IS USED.
ADDRESSES. COOPER & DUNLAM
STREET: 30 ROCKEFELLER PLAZA
STREET: NEW YORK
STATE: NEW 
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ATTORNEY/ACENT INFORMATION:
NAME: White, P. John
REGISTRATION BURBER: 23,678
REPRENCY DOCKER YNBER: 4266
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 177-9550
TELERAX: (212) 664-0525
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TYPE: amino acid
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PCT-US93-12586-4
              GENERAL INFORMATION:
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88.34; Score 1884; DB 1; Length 406;

Bert Local Similarity 99.34; Pred. No. 2.78-143;

Matches 356; Conservative 13; Mismatches 16; Indels 14; Gaps
Patent No. 576699
Patent No. 576699
Patent No. 576699
Patent No. 576699
CARREAT INFORMATION
CARREAD INFORMATION
TITLE OF INVENTION IN AN ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION IN DIA BY DESS THERROP
CORRESPONDENCE ADDRESS:
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30 ROCKEFELLER PLAZA
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US-08-446-822-4
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10112
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; Sequence 4, Application US/09555313B ; Patent No. 6506580

US-09-555-313B-4

PCT-US93-12586-4 ; Sequence 4, Application PC/TUS9312586

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61 SLAPADLLVSVLVMPPGAIBLVQDIWIYGEVFCLVRISLDVLLITASIFHLCCISLDRYY 120
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TITTE OF INVENTATION, Splicing variants of the human serotoninergic receptor
TITTE OF INVENTATION, Splicing variants of the human serotoninergic receptor
TITTE OF INVENTATION, Splicing variants of the formation of the series of th
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                                                                                       1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
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      Indels
      4
0; Mismatches
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Patent No. 6506580
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Best Local Similarity 95.2°
Matches 359; Conservative
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ORGANISM: Homo sapiens
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TITLE PO INVESTION: 50-114 and uses thereof, in particular for screening
TITLE PO INVESTION: 50-114 and uses thereof, in particular for screening
TITLE PO INVESTION: 50-114 and uses thereof, in particular for screening
TITLE RETENBROR: 50-50-130-130
TOTRED FILING DIE: 200-20-13
TOTRED FILING DIE: 200-20-13
PRIOR FILING DIE: 1997-11-28
PRIOR FILING DIE: 1997-11-28
STOR FILING DIE: 1997-11-28
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Pred. No. 7.1e-143;
0; Mismatches 0;
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Perent No. 6505580
Perent No. 6505980
Perent No. 650
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Best Local Similarity 96.2
Matches 359; Conservative
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Best Local Similarity
      SENERAL INFORMATION:
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ORGANISM:
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241 OMLORAGASSESRROSADGHSTHRWETETKAMTL.CITMCCCC.CWAPFYTNIVDPFID 300
227 OMLORAGASSESRROTADGHSTHRWETETKAMTL.CVIVACCPCRAPFYTNIVDPFID 286
227 OMLORAGASSESRROTADGHSTHRWETETKAMTL.CVIVACCPCRAPFYTNIVDPFID 286
       170 ---IEKRKFNHNSNSTFCVPMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAQQI 226
                                                                                                                                       301 YTVPGQVWTAFLWLGYINSGLNPFLYAPLNKSFRRAFLIILCCDDERYRRFSILGQTVPC 360
                                                                                                                                                                61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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TELECOMONICATION INFORMATION:
TELERPHONE: (212) 278-0400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,822
FILING DATE: UNDE 1, 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                361 STITINGSTHVLRDAVECGGQ 381
                                                                                                                                                                                                                                                                          347 STTTINGSTHVLRYTVLHSGQ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: White, P., John
REGISTRATION NUMBER: 28,678
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 338; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                   YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRFSILGQTVPC 360
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Query Match

Best Local Similarity , 88.7%; Pred. No. 4.16-134

Best Local Similarity , 88.7%; Pred. No. 4.16-134

Best Local Similarity , 88.7%; Pred. No. 416-134

Best Local Similarity , 88.7%; Pred. No. 416-134

Makenbes 138; Conservative 11; Mismatches 18; Indels 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/996,712A
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5472866
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ATTORENY/AGENT INFORMATION:
NAME: Hitle P. John
REGISTRATION (WHREE: 28,678
REBERENCE/DOCKET NUMBER: 4266'
TELECHOMANICATION (NOTORITION: TELECHOME: (712) 977-9550
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STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
                                                                                                                                                            361 STTTINGSTHVLRDAVE 377
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TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
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amino acid
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US-07-996-772A-2
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MEDIUM TYPE: Floppy
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TELEFAX: (
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61 SIAFADILUSVLVNAFGAIELVQDIMFYGEMFCLVRISLDVLLTASIFHLCCISLDRYY 120
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287 YTVPEKWHTAFLWLGYINSGLNPFLYAFLWKSPRAPLIILCCDERYRRPBILGGTVPP 346
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                                             Sequence 7. A APPILICATE ON PC/TUS9312586

GENERAL HISCORPATION

APPILICATE, SYNAPITO PRIMARCHITICAL CORPORATION

TITLE OF INVERTION: DAY ENCODING 5-HT4 SERCITONIN RECEPTORS

TITLE OF INVERTION: AND USES THERDEF

NUMBER OF SECURNES: 13 SHERDEF

CORRESSERS: COOPER & DUNHAM

STREET: 30 ROCKMEPLIER PLAZA

CITY: NEW YORK

STATE: NEW YORK

WEDIGHTER READLARE PORM:

WEDIGHTER READLARE PORM:
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ATTORNY, AGENT INFORMATION:
MADE: WHILE P. JOHN 198.679
BESISTENDATION UNMER: 28.679-A-PCT/JPW/TEP
PERSENDATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORM (212) 64-555
INFORMATION TO 64-555
INFORMATION TO 64-555
SEGUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12586
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IMW PC Computatible
COMPUTER: IMW PC Computer
STSTATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
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TYPE: amino acid
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                             CT-US93-12586-2
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RESULT 14
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TILLE OF INVENTION HOME BEACHING SHOWN HEATEN
THIS OF INVENTION HOMER: US/00/228,114
CURRENT APPLICATION NOMER: US/00/228,114
EMAILER APPLICATION NOMER: US/00/228,114
EMAILER PRINKO HOME: 1998-04-03
EMAILER PRINKO HOME: 1998-04-03
EMAILER PRINKO HOME: US/09,0772
EMAILER PLINKO HOME: US/09,0772
EMAILER PLINKO HOME: US/09,0772
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YTVPEXVATAFLMIGYINSGLAPFLYAFLAKSFRRAFLILLCCDDERYRRPPILGGTVPC 346
YTVPEXVATAFLMIGYINSGLAPFLYAFLAKSFRRAFLILLCCDDERYRRPPILGGTVPC 346
    OMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFID 300
                             YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
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Best Local Similarity 88.74; Pred. NO. 4.1e-134; Indels 14; Gaps
Matches 38; Conservative 11; Mismarches 18; Indels 14; Gaps
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ORGANISM: Rattus norvegicus
S-09-328-314-2
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307 WWAREMIGTINGGLAPFI, VAPLAKSPRAPLITICCODBRYRPSTIQOTPCSTTTIN 366
167 WWAREMIGSTNSGLAPPLYAFILNGSPRAPLITICCODBRYRPSTIGOTPCSTTTIN 236
167 WWAREMIGSTNSGLAPPLYAFILNGSPRAPLITICODBRYRRSTIGOTPCSTTTIN 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 RKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFILMVLAYYRIYVTAKEHAHQIQMLQRA 246
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RESULT 15

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Sequence 51, App. Sequence 493, App. Sequence 47, Appl. mence 2, Appl.
                                                                                                               Sequence 30, April
Sequence 90, April
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Sequence 5, April
Sequence 62, April
Sequence 64, April
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Sequence 8, Appli
Sequence 10, Appl
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Sequence 48, Appl
Sequence 24, Appl
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Best Local Similarity 96.5; Pred. No. 6.6e-186.
Matches 388, Conservative 0; Manatches 0; Indels 14
; Sequence 8, Application US/09989861
; Patent No. US20020081661A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gerald, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Sequence 4, Appl
Sequence 45, Appl
Sequence 446, App
Sequence 441, App
Sequence 411, App
Sequence 7, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
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Sequence 124, App
Sequence 18, Appl
Sequence 439, App
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2741.316 Million cell updates/sec
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11. (1992 6 (prodetal/) (pubbas/1807 purcova.pp;

21. (1992 6 (prodetal/) (pubbas/PCT NRW PUB.pp;

22. (1992 6 (prodetal/) (pubbas/PCT NRW PUB.pp;

23. (1992 6 (prodetal/) (pubbas/PCT NRW PUB.pp;

24. (1992 6 (prodetal/) (pubbas/1806 NRW Pub.;

25. (1992 6 (prodetal/) (pubbas/1806 NRW Pup;

26. (1992 6 (prodetal/) (pubbas/1806 NRW Pup;

27. (1992 6 (prodetal/) (pubbas/1809 PubCOMB.pp;

28. (1992 6 (prodetal/) (pubbas/1809 PubCOMB.pp;

2992 6 (prodetal/) (pubbas/1809 PubCOMB.pp;

2092 6 (prodetal/) (pubbas/1809 NRW PubCOMB.pp;

21. (1992 6 (prodetal/) (pubbas/1809 NRW PubCOMB.pp;

23. (1992 6 (prodetal/) (pubbas/1809 NRW PubCOMB.pp;

24. (1992 6 (prodetal/) (pubbas/1809 NRW PubCOMB.pp;

25. (1992 6 (prodetal/) (pubbas/1809 NRW PubCOMB.pp;

26. (1992 6 (prodetal/) (pubbas/1809 NRW PubcOMB.pp;

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26. (1992 6 (pr
                                                                                                                                                                                                                                                                                   August 5, 2004, 13:35:20 ; Search time 46.Seconds
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Copyright (c) 1993 - 2004 Compugen Ltd.
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4 UB-10-157-184

1 UB-09-25-567A-18

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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aximum DB seq length: 2000000000
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2133
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Match 1
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2042 2042 2042 2042 2043 2044 1954 1886 1879 1874 1872 1872 1872 1769 939

Oy 361 STITINGSTRIVEDN/BEGGGRPRISPLYAAQPSDT 402  Db 347 STITINGSTRIVEDN/BEGGGRPRISPLYAAQPSDT 388  RESULT 3  US-10-15'-031-124  US-10-15'-031-124  US-10-15'-031-124  SEQUENCE 144, Application US/10157031  PADLICANT: BARKONEN, N. K.  APPLICANT: VAROWATION, N. K.  APPLICANT: VAROWATION, N. F.  APPLICANT: ADARBORY, N. K.  APPLICANT: ADARBORY, N. K.  APPLICANT: ADARBORY, N. M.  APPLICANT: ADARBORY, N. M.  APPLICANT: ADARBORY, N. M.  APPLICANT: ADARBORY, N. M.  APPLICANT: ANGONOMES.  UNWARTORY FILM ADARBORY, US/10,1031  UNRERY PELING DAYE: X002-031  WORREY FILM APPLICATION WARREN: US/10,157,031  UNRERY PLING DE NOS 115  SOFTWARTORY FILM APPLICANT ANGONOMES.  WORREY PLING ANGONOMES.  WORREY FILM APPLICANT ANGONOMES.  WORREY FILM APPLICANT ANGONOMES.  WORREY FILM APPLICANT ANGONOMES.  WORREY FILM APPLICANT ANGONOMES.  WORREY FILM WORREY ANGONOMES.		RESULT 4  US-10-225-567A-18  Sequence 18, Application US/1025567A  POBLICANT INFORMATION: RESULT APPLICANT: Brown, Oseph P.  RESULT APPLICANT: Brown, Oseph P.  RESULTON: RESULT APPLICANT: Brown, Oseph P.  RESULTON: RESULT BROWN CALLED BROWN CONTROL OSEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECE! FILE REFERENCE: 1202-4-4  CURRENT FILING NATION. NATIONER: USL/10/225,567A  CURRENT FILING NATION: 2001-12-19
Db   61 SIAPADLIAYSULWPFGATELVQDIMIYGGWFCLVWTSLDVLTTASIPHLCCISLDRYY 120	Wishort 2  Wishort 2	0y         181 FIAIEKRENGNISSITCVPRVKPALTCSVVAPTIPELLMIATRITVTAKERHAOI 240           0b         170

PRIOR PRIOR APPLICATION NUMBER: 60/257,144  NUMBER 05 850 JD NOS: 2292  SECTIANS 18	11, 00, 00, 00, 00, 00, 00, 00, 00, 00,
9 301 YTVPQQVMTAFLALGYINSGLNPPLYAFLKKSFRAFLILLCCDDERYRRSELIGGTVPC 360 289 YTVPQQVMTAFLALGYINSGLNPPLYAFLKSFRAFLILCCDDERYRRSELIGGTVPC 346	
y 361 STTINGSTHVIABAVEGGGGRESGCHPPATSPLVAGPSDT 402	
D 347 STTXINGSTHVLKUAVECGCGMESQCHFPATSFLVAAQFSDT 388 ESULT 5	FRIOR FILIDA DATE: 2001-03-07 FRIOR APPLICATION WWEEE: US 60/278,927 FRIOR FILIDA DATE: NOWEE: US 60/278,927 FURBROR FILIDA DATE: NOWEE: US 60/278,927

61 SLAPADLLVSVLVMPPGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 61 SLAFADLLVSVLVMPFGAIELVQDIWYYGEMFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 121 AICCOPLVYRNKMTPLRIALMIGGCWVIPTFISFLPIMOGWNNIGIIDLERSLNQGLGQD 180 121 AICCQPLVYRNXOTPLRIALMIGGCWVIPMFISFLPIMQGWNNIGIVDL------ 169 9 1 MDKIDANVSSKEGFGSVEKVVLITFLSAVILMAILGNLLVMVAVCRDRÇLRKIKTNYFIV 60 1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV Indels 14; Gaps Query Match
Best Local Similarity 9:04; Pred. No. 1.4e-176.
Matches 370; Conservative 8; Mismatches 10; Indels 14
Matches 370; Conservative 8; Mismatches 10; Indels 14 SOFTWARE: Patentin version 3.0 SEQ ID NO 3
1 LENGTH: 388
1 TYPE: PRT
1 ORGANISM: CAVIA PORCELLUS
US-10-022-771-3 임 셤 ò 임 ઠે ò 요 ò

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BUDICARE LINGOMETICAN SOLUTION SOL

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1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60

Ouery Match 95.5; Score 2037; DB 11; Length 388; Best Local Similarity 96.3; Pred No. 2e-184; Matches 387; Conservative 0; Mismatches 1; Indels 14;

TYPE: PRT ORGANISM: Homo sapiens

8-09-826-509-439

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Sequence 416, Application UB/09826309
Publication No. US20030204073A1
SUBSEAL INFORMATION: Lehmann-Publiman, Karin
APPLICANT: Lehmann-Publiman, Karin
APPLICANT: Lim. 1-Lim. 1-Li
                                                                                                                                                                                                          Spelicuri. Conklin: Bruce R.
TITLE OF INVENTION: Selective Target Cell Activation By
TITLE OF INVENTION: Selective Target Cell Activation By
TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
FILE REFERENCE. UCL. 048CTP2
CURRENT PAILLY CATION NUMBER: US 0.04.1446
FRIOR PRING TARGET TO 030-02-05.446
FRIOR APPLICATION NUMBER: US 09/341,446
FRIO
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                                             Sequence 23, Application US/10318661
Publication No. US20030167476A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-318-661-23
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APELICARY MEINDANK, RICHARD I.
ITILE OF INVERTION IN MENOCAIDS SHITA SECOCOMIN Receptors And Uses
ITILE OF INVERTION IN MENOCAIDS SHITA SECOCOMIN RECEPTOR AND USES
CURRENT PAPLICATION NUMBER: US/09/999.861
CURRENT PAPLICATION NUMBER: BALLER APPLICATION NUMBER: 09/128,134
PRIOR FILMS OFFICE MELLER FILMS OFFE: 1999-11-2
PRIOR PELLOR OFFICE MELLER PELLOR OFFE: 1999-11-2
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Patent No. US20020081661A1
GENERAL INFORMATION:
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287 YIVDOOWIAFIMLOYINGGLNPFINAFINSFRRAFIIILCCDBRYRRFSILGGTYPC 346
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                                                                                                                                                                                       Indels 14;
                                                                                                                                                            Length 387;
                                                                                                                                                          Score 1874; DB 11;
Pred. No. 5.5e-169;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 443, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR PLILING PARE: 1998-10-13
WYMER OF SEQ ID NOS: 589
SOFWARE: Patentin Version 2.1
SEQ ID NO 438
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STTTINGSTHVLRDAV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 STTTINGSTHVLRYTV 362
                                                                                                                                                          Query Match
Best Local Similarity 95.5%;
Matches 359; Conservative
                                                                                               ORGANISM: Homo sapiens
S-09-826-509-436
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                                                                                            TYPE: PRT
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1 MDXLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYPIV 60

Gaps

14;

Indels

Score 1873; DB 11; Pred. No. 6.3e-169; 0; Mismatches 1;

Ouery Match 87.8%; Best Local Similarity 96.0%; Matches 358; Conservative C

TYPE: PRT ORGANISM: Homo Bapiens S-09-826-509-443 Length 360,

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PERICONIT Lebmann-Bruinsma, Karin
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95.0%; Pred. No. 8.4e-169;
iive 0; Mismatches 5;
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Publication No. US20030204073A1
GENERAL INFORMATION:
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Matches 358; Conservative
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s Sequence 2. Application US/0998961 Pacar No. USCONDOBLEGALA PAPLICANT. Gerald, Christophe APPLICANT. Gerald, Christophe APPLICANT. Standbark, Horesa APPLICANT. Branchek, Horesa APPLICANT: Branchek, Horesa APPLICANT: Branchek, Richard L. TITLE OF INVENTION: Thereof. FILE REFERENCE, 4266-A22-P71. CURRENT APPLICATION WANGER: US/09/999.661 CURRENT PELLING DATE: 2001-112. PAPLICATION WUNGER: 09/328.314	PRIOR PILING DATE: REALIER FILING DATE: 1998-04-03 PRIOR PILING DATE: REALIER FILING DATE: 1999-112-28 PRIOR PILING DATE: REALIER FILING DATE: 1993-112-24 PRIOR PILING DATE: REALIER FILING DATE: 1992-112-24 PRIOR PILING DATE: REALIER FILING DATE: 1992-12-24 NUMBER: PALENTIN USE: 19 FORTHARE: PALENTIN FILING DATE: 1992-12-24 NUMBER: OF 100 10 NOS: 19 FORTHARE: PALENTIN VET: 2.1 FORTHARE: PALENTIN VET: 2.1 FORTHARE: PALENTIN VET: 2.1 FORTHARE: PALENTIN VET: 3.1	Query Match  82.94; Score 1769; DB 9; Length 387;  Best Local Similarity 88.74; Pred. No. 56-159;  Matches 338; Conservative 11; Mismatches 18; Indels 14; Gaps 1;  MATCHES 338; CONSERVATIVE 11; Mismatches 18; Indels 14; Gaps 1;  OY INDILIDANUSEBEGFGSVERVILTFERSTVILAMILGALLAWAVCENGLERITRINFITY 60  DE IMPLIANUS MATCHEN TABLE 1	61 SLAFADLASVIANASCATELOOD INFOGRACIANT	Qy 181 FHAIEKRKENQNSNSTYCVFWANKEYA.TCSVVAFY.IPFLLAVLAVYB.TYTAKEHAGI 240  10IEKRKEHIRSNSTFCVFWANKFYA.TCSVVAFY.IPFLLAVLAYR.IYTAKEHAQI 226	0y 241 QMQBAAGSESSRPQBADAGTHRANTETAKTACTISCECCCAAFFFYTUVDPPLD 300	Oy 301 YTYPGOVTRE-M-GYINSGLNEPT-ARELYSERRE-LILLICODERREAD LICOPYC 360 Db 287 YTVPEKWYNEPL-M-GYINSGLNEPLAPLAFIANSFRIAR-LILLICODERRYKREPILGOTVPC 346	Oy 361 STTTINGSTRVLARAVECOGO 381  Db 347 STTINGSTRVLARYTVLABGO 367	RESULT 14 [12:09-9861-15 - Semmerce 15 _ Arm its/nessa64	Patent No. US20020081661A1 ; GENERAL INFORMATION: ; APPLICART: General, Chriscophe	A PAPLICANT: BATTLE, Fall K.  A PAPLICANT: Barnebe, "Receat I.  TITLE TO TAVETHER TON: "The caced dies 5-HT4 Serotonin Receptors And Uses  "TITLE TO TAVETHER TON: "The caced dies 5-HT4 Serotonin Receptors And Uses	PILE REFERENCE: 4.56-74.2-77.10 CURRENT APLICATION NUMBER: 105/09/861 CURRENT FILING DATE: 2001-11.19
Gy         241 OWLORAGASSESRADGISTHENGTERKANTHCHINGCECLCMAPPETHINDPPED 300           Db         227 OWLORAGASSESRAGSADGISTHENGTERKANTHCHINGCECLCMAPPETHINDPED 266           Gy         301 YMYCOWATERKINGTHSCLAFTANTERRERABLILLCCDDBRYREPSILGQTVPC 360           Db         287 YMYCOWATERKINGTHSCLAFTANTHNSFRARELLILCCDDBRYREPSILGQTVPC 346           GY         361 STITLINGSHWILDDAW 377           Db         347 STITLINGSHWILDDAW 377           Db         347 STITLINGSHWILDSGTB 363	REGULT 12  BUB-09-26-509-445  JG-09-26-509-445  JG-09-26-509-445	PRIOR APPLICATION NUMBER: 60/195,747 FRICK FILING WATER 2000-04-07 FRICK FILING WATER: 09/10,496 FRICK FILING WATER: 09/10,496 FRICK FILING WATER: 1998-10-13 NUMBER OF SEQ ID NOS: 599 5. SOFTWARE: Patentin Version 2.1 SEQ ID NO 445 TYPE: PRI	. ORGANISK: Home captions US-09-264-509-465 US-09-284-509-465 US-09-284-509-465 US-08-10-284: DS-08-18-18-18-18-18-18-18-18-18-18-18-18-18	Cy 1 MDKLDANYSZEEGFGSVEKVYLITFLSTVILAMILGALLAWVAVGNBGLRKIKTNYFTV 60  DD 1 MDKLDANYSZEEGFGSVEKVYLITFLSTVILAMILGALLAWVAVCADEGLRKIKTNYFTV 60	Cy 6.1 SLARADILANSTANDRASEARINGOINTGEPELANDRAINLITAISTERICTSLARYY 120  Db 6.1 SLARADILANSTANDRASEARINGOINTGEPFCLARISEDVILITASIFERICCISLERYY 120	Oy 121 AICOCOPAVENINFEZ AAAACOONPET SEPENANNICIIERSENOGIGOD 180 Db 121 AICOCOPAVENINFEZ AAAACOONPET SEPEN PROGNINICII D	Cy 181 FPLERKERNONSINETCRPMENTATICSUPARTICSUPARTICINTATION 1210 - 110 IERGREROGNISHSTOCKPMENTATICSUPARTICSUPARTICINTI	Oy 241 ONLORAGSESERPODESTHERMENT CLINGCECCANETYTINDED 300 227 ONLORAGASESERPOSADGHSTHENDETRIAKKTLCIINGCECLCANEFYTHIUDEFID 266	Oy 301 YYVOOWTAPAACAYNGAAPPLAKKRRBAALIACCDDBRABSTLOOPC 360 Db 287 YYVOOWTAPAACAYNGAAPPLAKERPELAKKRBAAPILICCDDBRARRESILOOPUP 346	Oy 361 STTINGSTHVLBANEGGGGRESOCHP 386  Db 347 STTINGSTHVL	RESULT 13

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307 VWTAFLMLGYINSGLMPPLANEFRBAFLIILCCDDERYRHPSILGQTVPCSTTTIN 366
167 VWTAFLMCYNSGLMPPLYAFLNISFRBAFLIILCCDDERYRHSFLGOTVPCSTTTIR 226
17 VWTAFLMCYNSGLMPPLYAFLNISFRBAFLILLCDDERYRHSFLGOTVPCSTTTIR 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 RKFNQNSNSTYCVFMVNKPYAITCSVVAPYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 RKENONSINSTYCVEMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOIQMLQRA 106
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PRIOR APPLICATION WINNERS. PARLIER RAPLICACION WUMBER: 09/326,314
PRIOR PILLING DATE: BARLIER FILING DATE: 1998-04-09
RICH FILING DATE: BARLIER FILING DATE: 1998-04-09
RICH RELIAGO NUMBER: PARLIER RAPLICATION WUMBER: PCT/US9/1/2286
RICH FILING DATE: BARLIER FILING DATE: 1993-142-23
RICH FILING DATE: BARLIER FILING DATE: 1992-12-24
NUMBER: 05D IN NOS: 19
SEQ TOWNER: PARCHIER PLING DATE: 1992-12-34
SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 1239; DB 9;
Pred. No. 5.3e-109;
0; Mismatches 2;
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al Similarity 93.6%;
234; Conservative
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S-09-989-861-15
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Best Local Similarity
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Matches
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127 LVYRNKATPLRIALMLGGCWVIPTFISFLDIMGGWNNIGLIDLERSLANGGLGQDFHAIEK 186

Query Match
44.0t; Score 939; DB 9; Length 178;
Best Local 78 imilarity 92.2t; Pred No. 9.1s-81; Indels 14; Gaps Matches 17; Conservative 0; Missucches 1; Indels 14; Gaps

TYPE: PRT ORGANISM: Homo sapiens S-09-989-861-6

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WINGER OF SEQ 1D NOS: 19

SEQ 1D NOS: 19

SEQ 1D NOS: 19

Sequence 6, Application US/09989861 Patent No. US20020081661A1 GENERAL INFORMATION;

3-09-989-861-6

Search completed: August 5, 2004, 13:41:22 Job time : 48 secs 167 WIAFLWLGYIN 178

307 VWTAFLWLGYIN 318

187 RKENQNSNSTYCVEMVNKPYAITCSVVAPYIPPIIMVLAYKIYVTAKEHAHQIQMLQRA

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

## SUMMARIES

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:	3	555549	S55550	S66493	S66495	S664B7	A55886	I50475	A56849	151659	DYHUD1	147217	151661	A25896	872168	B56849	QRHYB2	DYHUDS	A41271	DYRTD1	151660	JQ1278	I53040	\$12591	C55886	S00260	B55886	836794	QRHUB2	JH0449 .
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Suery	March	4.4	82.9	35.4	32.8	30.4	28.9	28.6	27.7	27.6	27.3	27.3	27.2	26.9	26.9	26.6	26.5	26.4	26.4	26.4	26.3	26.2	6.1	26.0	25.9	25.8	5.8	5.7	5.6	9.6
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į	Score	1886	1769	755	700	648	617	610	591.5	588.5	582.5	581.5	580	574	573.5	568	999	563.5	562.5	562.5	562	559	556	554.5	553.5	550	250	549	547	545.5
esult	20	1	63	e	4	'n	9	7	80	đ	10	11	12	13	14	15	91.	17	18	19	50	21	55	23	24	25	56	27	28	53

beta-4C-adrenergic	beta-2-adrenergic	beta-1-adrenergic	beta 1 adrenergic	histamine H2 recep	dopamine D1-like r	serotonin receptor	hypothetical prote	histamine H2 recep	G protein-coupled	dopamine receptor	serotonin receptor	serotonin receptor	alpha-1A-adrenergi	alpha-1A-adrenergi	serotonin receptor
A55044	S10855	QRHUB1	153053	JC4120	268780	A48881	T25689	A39008	JC5042	844275	A47519	S36402	JH0447	139369	JH0315
~	~	н	N	N	N	~	~	7	0	N	N	~	N	N	N
428	418	477	480	359	385	445	420	359	476	511	448	448	501	572	422
25.3	25.3	25.2	25.1	24.9	24.5	24.4	24.3	24.2	24.2	24.1	24.1	23.7	23.4	23.4	23.3
539.5	539	537.5	535	531.5	523.5	519.5	517.5	516,5	516	514.5	513	909	498.5	498.5	496.5
30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

#### ALIGNMENTS

283366

NiAlectrate names 5-HT receptor 4b
Cloates 10-Octo5359 Augustec\_mevialon 03-Nev-1995 #text\_change 24-Nev-1999
Cloates 10-Octo5359 Augustec\_mevialon 03-Nev-1995 #text\_change 24-Nev-1999
Cloates 10-Octo5359 Augustec\_mevialon 03-Nev-1995 #text\_change 24-Nev-1999
Received 19-Octo5359 19-Octo5359 19-Octo5359 PMID:7796807
A.Reference number: 855549 MID:95317299 PMID:7796807
A.Reference number: 855549

A.Foleute: prejainlary
A.Foleute: prejainlary
A.Foleute: prejainlary
A.Foleute: Cype: mRNA
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A. Ajcreesion: Sefetys
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A. Ajcreeura muclaci acid sequence not shown
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A. Ajcole

ä 9 1 MDXLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 16, Indels 14; Gaps Query Match 88.4%; Score 1886; DB 2; Length 406; Best Local Similarity 89.5%; Pred. No. 6.1e-16. Matches 357; Conservative 12; Mismatches 16; Indels 1º Matches 357; Conservative 12; Mismatches 16; Indels 1º à

120 61 SLAFADLLVSVLVNAFGAIELVQDIWFYGEMFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 121 AICCOPLYKNINGTPLRIALAGGWYIPTFISFLÞIMGGWNNIGIIDLERSLNQGLGOD 180 181 PHAIBKRKFNQNSNSTYCVFNVNKPYALTCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI 240 61 SLAFADLLVSVLVMPFGAIBLVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY ò g ઠે ď 셤 ક

226 QMLORAGASSESRPQASTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300 170 ---IEKRKFNHNSNSTFCVFWVNKPYAITCSVVAFYIPFLLAMVLAYYRIYVTAKEHAQQI 241 g ò

ansmembrane pr

A, Molecule type: mRNA A, Rose the Color of	Section to receptor 44 - pig (fragment)  Signaturate names: 2-pydroxytrpatins receptor 44 (5-HT84A)  C, Species: Sim sercia domestica (domestic pig)  C, Date: 22-(0-1.95 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000  C, Accession: Séd459  R,UJIENC, C, Schmack, K, Kalkman, H.O.; Luebbert, H.  FERS Lett. 70, 215-221, 1395  A,Rittle Expression of Sectoon in receptor manks in blood vessels.  A,Reference mucher: Séd497, WID1-93585799; PMID: 565890  A,Rosession: Séd497, WID1-9358799; PMID: 565890  A,Rosession: Séd497, WID1-9358799; PMID: 565890  A,Rosession: Séd497, WID1-9358799; PMID: CAB8199.1; PID1-9984245  C,Saptones: PMED: 22-87; PMED: 22-87; PMED: CAB8199.1; PID1-9984245  C,Saptones: Restrict receptor  C,Reyords: neurotransmitter recept	RESULT 5 56487 86487 86487 86487 86487 86487 86487 86487 86487 86488 864
Oy 301 YTVPGOWTAPLHIGTINGGAMPELARIKKERBAPLIILCCDERYRRSGILGGTVPC 360  Db 287 YTVPEKWATAFLHIGTINGGAMPELARIKKERBAPLIILCCDERYRRSGILGGTVPC 346  OY 315 STTINGSTHIADDVBCGGAPERGCHERAPLARILITCCDERYRRSPELIGGTVPC 346  Db 347 STTINGSTHIADDVBCGGAPERGCHERAPLANDP 399  SESSUIT 2  SESSUIT 2  SESSUIT 2  SESSUIT 2  SESSUIT 2  SESSUIT 2  SESSUIT 3  SESSUIT 3	Query March   Garey March	Side 3. Section receptor 4 - human (fregment) NiAteriare mases: 5-hydroxyrryptemine receptor 4 (5-HTR4) NiAteriare mases: 5-hydroxyrryptemine receptor 4 (5-HTR4) Signer: 28-correst mans section (ann) Cipperia Hono sapleme (ann) Aither Expression (ann) Aithers (ann) Aither

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Coppedies Carassis autre (goldfish)
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Riversis Des Mancher (goldfish)
Riversis Des Mancher (goldfish)
Arritles (Coning and Characterization of a truncated dopamine Di receptor from goldfish)
Arritles (Coning and Characterization of a truncated dopamine Di receptor from goldfish)
Arytles (Coning and Characterization of a truncated dopamine Di receptor from goldfish)
Arytles (Coning and Characterization of a truncated dopamine Di receptor from goldfish)
Arytcession: ISO475, WIDD:9408471; PMID:8264547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NFFVISLAVSDLLVAVLVMPWKAVTEVAGFWPFG-AFCDIWVAFDIMCSTASILNLCVIS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 NYFIVSLAFADLLVSVLVMPFGAIBLVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCIS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 LDRYYAICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMOGWNN---IGIIDLERS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 LNGGLGODFHALEKRKFNONSNSTYCVFMVNKPYALTCSVVAFYIPFLLMVLAYYRIYVT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AKEHAHQIQMLQRAGASSESRPQS----ADQHSTHRM--RTETKAAKTLCIIMGCFCL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 CWAPFFVTNIVDPFIDYTVPG-----QVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CWLPPFILNCWVPFCKRTSNGLPCISPTTFDVFVWFGWANSSLNPIIYAF-NADFRRAFA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAVLDLNLTTVIDSGFMESDRSVRVLTGCFLSVLILSTLLGNTLVCAAVTKFRHLRSKVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dopamine receptor-like protein D14 - Japanese pufferfish
C.Species: Fugu rubripes (Japanese pufferfish)
Peter :7-oc-1999 #sequence_revision 27-oc-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDKLDANVSS - - EEGFGSVEKVV - LLT - - FLSTVILMAILGNLLVMVAVCWDRQLRKIKT
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A)Cross-references: GB:X80174; NID:G1204089; PIDN:CAA56455.1; PID:G1204080
C, Siparefamily: vertebrese rhodopsin
C, Kaywordes: neurostrammitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L08602; NID:g212949; PIDN:AAA16322.1; PID:g212950
C;Superfamly; vertebrate rhodopsin
C;Keywords: nautoctanemitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
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Genomics 25, 456-446, 1995
A.Title: Analysis of the dopamine receptor family in the compact
A.Reference number: A56849; MUID:95309911; PMID:7789977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.6%; Score 610; DB 2; Length 36 Best Local Similarity 38.4%; Pred. No. 1.88-47; Matches 149; Conservative 65; Mismatches 118; Indels
362 ETVSINNN------GAVFSSQHEPKGSSP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
Residues: 1.363 <FRA>.
                                                                                                                                                                                                                                                                dopamine D1 receptor - goldfish
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|Note: authors translated the codon MET for residue 427 as 11e, and ACC for residue 440
| Superfamily: vertebrate the rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jDemchyehyr, L.L.; Sugamori, K.S.; Lee, F.J.S.; Hamadanizadeh, S.A.; Niznik, H.B.
Shol. Chem. 270, 4005-4012, 1935 Cloning and characterization of three pharmacological
filtle: The dopamine Dr eccepto. Cloning and characterization of three pharmacological
effectence mulec: ASSB86; WOIL:95181368; PMID:7876148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 AIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPPLLMVLAYYRIYVTAKEHAHQIQM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 -IEKRKFHQNSNSTYCIFWVNKPYAITCSVVAFYIPFLLMVLAYWRIYVTAKEHAHQIQM 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 IWIYGEVPCLVRISLDVLLTIASIPHLCCISLDRYYAICCQPLVYRNKWTPLRIALMLGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 FWPFGS-FCNIWVAFDIMCSTASTINLCVISVDRYWAI-SSPRYERRWTPKAAFIMISV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AWTLSVLISFIPVQLNWHKATTTSFLDLNASL-QGISMD------NCDSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNKPYALITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRA-------GASS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPPIDYTVPGQ---- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 SMDCQOPESNFKMSFKRETKVLKTL&VIMGVFVCCMLPFFVLNCMIPPCEPTQDSKGAEA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 FCINSTTEDVFIWFGWANSSLNPIIYAF-NADPRKARFSTLLGC---YRLCPMSGNAI-- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCQPLVYRNKOMTPLRVAVLLAGCWAIPVLISFLPIMGGWNIGITDL------47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 CWVIPTFISFLPIMOGWN---NIGIIDLERSLNOGLGODFHAIEKRKFNONSNSTYCVFM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 FLSTVILMAILGNLLVMVAVCMDRQLRKIKTNYFIVSLAFADLLVSVLVMPFGAIELVQD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Cross-references: EXBL: 248175; NID:9984242; PIDN: CAA88198.1; PID:9984243; Superfamily: vertebrate schoologsin
; Superfamily: vertebrate schoologsin
; Keywords: neurostranemitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                   Length 137;
                                                                                                                                                                                                                                                                                                                                                   Onery Match 30.4%; Score 648; DB 2; Length 137
Best Local Siniarity 80.8%; Pred. No. 2.3e-51;
Matches 122; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary, nucleic acid sequence not shown kholecule type: DNA kholecule type: DNA kholecule type: DNA kholecule type: 1-450 cDEA kholecule type: DNA kholec
                                  Status: preliminary; nucleic acid sequence not shown; Wolecule type: mRNA
Rolecule type: mRNA
sesiduse: 1-137 <ULL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LORAGAPAEGRPPSADQHSTHRMRTETKAAK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 LORAGASSESRPOSADOHSTHRMRTETKAAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 36.49
Matches 143, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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dopamine receptor D1 - human
(C.Species: Homo eapiems (m.z.n)
C.Baceis: Jace. 1992 Steequence revision 31-Dec.1992 #text_change 22-Jun-1999
C.Accession: S1377/ S1376: Š11379
R.Zhou, Q.Y. Grandy, D.K.; Thambi, L.; Kushner, J.A.; van Tol, H.H.M.; Cone, R.; P
Nature 347, 74-60, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Cross-references: DMBL1X59897
R. Descript, J. A.; Fizences: DMBL1X59897
Nature 347, 72.76, 1990
Nature 347, 72.76, 1990
A.Fitler Nolecular cloning and expression of the gene for a human D(1) dopamine rec.
A.Fitler enumber: S11376; MUID:90370093; PMID:2144334
A.Reference number: S11376; MUID:90370093; PMID:2144334
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A; Resedues 1-446 MEB-155760; MID:g30396; PIDN:CAA39286.1; PID:g30397
A; Cross-references: ENBL:X55760; MID:g30396; PIDN:CAA39286.1; PID:g30397
A; Cross-references: ENBL:X55760; MID:g30396; PIDN:CAA39286.1; PID:g30397
K; Sunmahara, R.K.; MixIII, H.E.; Weilner, D.M.; Stormann, T.M.; Brann, M.R.; Kennedy, Ngcure 437, 00-031, 1990
A; Fiftle: MixIII dopesine OII; receptor encoded by an intronless gene on chromosome 5 A; Rofference number; S11379; MUID:90370955; PMID:197540
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288 FILNCIVPFCDPSLTTSGTEPPCISSTTPDVFVWFGWANSSLNPIIYAF-NADFRKAFSN 346
                                                    340 ILCCDDERYRRPSILGOTVPCSTTTINGSTHVLRDA-VECGGGWESQCHPPATSPLVAAQ 398
                                                                                                    347 LLGC----YRLCPTSNNII--ETVSINNNGAVYSCQQEPKGSIPNECNLVYLIPHAIIC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 SLAVSDLLVAVLVMPWKAVABIAGFWPFGS-FCNIWVAFDIMCSTASILNLCVISVDRYW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 NTSAMDGTGLVVERDFSVRILTACFLSLLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Title: Cloning and expression of human and rat D(1) dopamine receptors. A.Reference number: S11377; MUID:90370094; PMID:2168520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: DNA
A.Resaidnes: 1.446 - SNA
A.Coogs-reference: GB:X55758; NID:g288331; PIDN:CAA39284.1; PID:g288932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:125240; OMIM:126449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-446 <ZHO>
                                                                                                                                                            399 PSD 401
                                                                                                                                                                                                            401 PED 403
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                                                                                                                                                                                                                                        60 WKAATEIMGFWPFGE-PCNIWVAFDIMCSTASIINICVISVDRYWAI-SSPFRYERKOTF 137
                                                                                                                                                                                                            76 PGAIELVQDIWIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRYYAICCQPLVYRNXMTP 135
                                                                                                                                                                                                                                                                                                                136 LRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIBKRRFWQNSNS 195
                                                                                                                                                                                                                                                                                                                                                    196 TY-----CVPMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                248 ASSESRPQ----SADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 BSAQNRHSSMGNSLSMESECSFKMSFKRETKVLKTLSVIMGVFVCCWLPFFILNCMVPFC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 FADLLUSVLVMPFGAIELVQDIMIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 VSDLLVAVLVMPWKAVAEIAGFWPFG-FFCNIWVAFDIMCSTASILNLCVISVDRYWAI- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWN---NIGIIDLERSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 SSPERYERKATPKVAFIMIGVAWTLSVLISFIPVQLNWHKAKTTSFFÖLNITLH----- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 FHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAPYIPFLLMVLAYYRIYVTAKEHAHQI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 -------DRTMDNCDSSLNRTYAISSSLISFYIPVAIMIVTYTRIYRIAAKQIRRI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 OMLORAGA-----SSESRPOSAD-QHSTHRMRT----ETKAAKTLCTIMGCFCLCWAPF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 FVINIVDPFID-----YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLI 339
                                                                                                                                        16 SVEKVVLLT------FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SMDEDVILLTERESSFRVLTGCFLSVLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVISLA 66
                                                                                                            16 SVEKVVLLTFLSTVILMAILGNILVMVAVCWDRQLRKIKTNYFIVSLAFADLLVSVLVMP
                                                        47, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DY------TVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Onery Match
27.6%; Score 588.5; DB 2; Length 451;
Best Local Similarity 34.5%; Pred; No. 24-45;
Matches 146; Conservative 64; Mismatches 150; Indels 63;
        Length 459;
    Omery Match 27.7%; Score 591.5; DB 2; Length 4 Best Local Smilarity 37.0%; Pred. No. 1.1e-45; Matches 130; Conservative 60; Mismatches 114; Indels
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121 124 125 126 127 127 127 127 127 127 127 127 127 127	12 AICODUNDRARATE AIALIGACHIPEISPICHOGNNIGIDE ESSANGGO 180 12 AI-GSPETKERKHPEADLIGAUPTE SPETCHOGNNIGIDE ESSANGGO 180 12 AII-GSPETKERKHPEADLIGAUPTE SPETCHOGNNIGIDE ESSANGTOOD 180 181 PHAIEREKENDRARATE SVATENDRARATE SPETCHOLATE SPETCH 182 183 AII-CHORAGASSE CONTRACT SPETCH SPETCH SPETCH 182 223 ALBANTAN COTTAGES SERVER SPETCH CONTRACT SPECCH 286 224 ALBANTAN COTTAGES SERVER CONTRACT SPETCH S

OY B6 WIYGEVFCLWRYSLDVLL/TASIFHLCCISLDRYYAICCOPLYRWRPERFALMIGGC 145  DD 107 WIMGSFLEGGWISLDVLC/TASIFILCYIAIDRICALI - TSPERFGSLMTRARAKVLICTV 165  OY 146 WVIPTFISTPINGGRANIGIIDLERSLNOGLGOPHAIEKAKRNONSHSTYCVPMWNKP 205  DD 166 WAISANSFLEIMWHW	OY 265 -MRIETKAAKILCIIMOCECLCHAPEVINIVDPEIDYTUPGOUNTAELMIGYI 317  256 SFRRETKULKILSVIMOVUYCHUPEPLAIOUNDPCRLEPAAPCVSDTTFSVFUWFGWA 315  QY 318 NSGLAPEVINFLUKSPRILILCODENYRRR8 352  DD . 316 NSSLAVIYAR-MADEKAESTILGG-SRYCKTS 347
Qy 206 YAITCSVVAPTIPELLAWIATYRIVTAKEHAHOIQHLQBAGASSESRPQ255  Db 207 YAIASSILISTPULLIHITYPERAKQTACKGGRPWGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RESULT 15 BG6899 GOPANIE zeeptor-like protein DL - Japanese pufferfish C;Speties: Ryugu tubripes (Japanese pufferfish) C;Date: 27-Oct-1995 Heavy Gopanese pufferfish) C;Date: 27-Oct-1995 Heavy Gopanese pufferfish) C;Accession B66899 R;Macrae A.D.; Berenner, S.
Oy         310 AFUNCATINGGLAPPLYAPINKSPRAMPLIILCCDBRYRRESILOGUVCSTTTIN 366           Db         327 FFWLLDINGCREAPINC-RSDDRAMPRELIILCCBRAUMCGOPAULCGFFITTIG 385           Oy         367 GSTHVLEDNARGCGGGGGG 387           Db         386 SPEILSPGGTM-SDCM 399	Genomics 25, 416-446, 1959 A.Title: Analysis of the dopamine receptor family in the compact genome of the puff A.Reference mumber: Assasy MUID:95309311; PMID:779937 A.Reference: Assassy MUID:77909311; PMID:77909311; PID:91204095 C.Superfemily: Vertee-femere: GE:80177; MID:91204094, PIDN:CAASs457.1; PID:91204095
RESULT 14 57210 14 57210 14 67210 14 67210 16 67210 16 67210 17 67	Veryords: neutotransmices receptor 26.64; Score 568; DB 2; Length 463; Dacry Match Watch 134; Pred. No. 1.56-43; Tidels 76; Gape datches 138; Conservative 57; Minmatches 131; Indels 76; Gape 26 ISTVILHARIGATIVNIVNIVONSRIKKTNIVETUSEAPADLINSVIVMPFORELEVADI 1
Authin: BioDPNy Acta Juot, 1-22, 1998 Altitle: Cloning and Sequence analysis of a hypothalamic cDNA encoding a D(1c) dopamine Altitle: Cloning and Sequence analysis of a hypothalamic cDNA encoding a D(1c) dopamine Altitle: Cloning and Sequence analysis of a hypothalamic S72168 Altitle: Cloning and S72168 Alti	a & a
A;Cross-references: EMBL:X81969; NID:9603868; PIDN:CAAS7494.1; PID:9603869 (S)upperfamily: Vertebrate indoppin (S)upperfamily: Vertebrate indoppin (S,Keywords: G protein-coupled receptor; g)lycoprotein; lipoprotein; neurotransmitter rece (F,Keywords: G protein-coupled receptor; g)lycoprotein; lipoprotein; neurotransmitter rece (F,Keywords: G protein-coupled receptor; g)lycoprotein; lipoprotein; ransmembrane feature predicted (FML) (F)10.10.10.0main: transmembrane feature predicted (FML) (F)10.11.10.0main: transmembrane feature predicted (FML)	04   05   05   05   05   05   05   05
F.135 - 7 / Voomain: Lanaument.ane Pasture pelliced (1795) P.136 - 21 / Voomain: Lanaument.ane Basture predicted (1795) P.136 - 21 / Voomain: transment.ane Basture predicted (1796) P.136 - 238 / Voomain: transment.ane Basture predicted (1797) P.136 - 238 / Voomain: transment.ane Basture predicted (1797) P.136 - 238 / Voomain: gite: phosphate (1797) (covalent) #status predicted F.1310 / Staff binding site: phosphate (Ser) (covalent) #status predicted F.1340 / Sinding site: phosphate (Cys) (covalent) #status predicted	8 8 8 8
Ouery Match 26.94; Score 573.5; DB 2; Length 386; Best Local Similarity 38.94; Pred. No. 3.96-44; Best Local Similarity 28.94; Pred. No. 3.96-44; Best Local Singarity 8.94; Pred. Niematches 119; Indels 37; Gaps 7;	Db 318 IFWF04NNSLAPITAL ANDFRAFTTILGCSRF
Oy 26 LSTVILMALIGNILWWANCHDROLRKITKTNYFIVSIAPADLILVSVINMPPRATELVQDI 85  12 LSTILVSLIMALIGNILWMANTEN	
Oy 86 WIYGEVPCLVRFISLDVLLTTASIPHLCCISLDRYYAICCOPLVRWRTPLRIAIMLGOC 145 Db 102 WIFG-AFECTWVVPINCOFALIHICLISMRWAI-SEPPRERRITERECEMIGNA 159	Saarch completed: August 5, 2004, 13:35:17 JOD Lime: 18 secs
OY 146 WUPTEISFLPIMOCHANICIIDLERSIAYQICQDEHAIBKGKFNQNSNSTYCVFWYNKP 205  160 WILSVILISFUQUANKHARQ REFIDEOCHAIRT 195	
OY 206 YAITCSWAPYIPPLAMTAYYRIYYTAKEHAHOIOMLORAGASSBRPGSADGHSTHR-264 Db 196 YAISSELISETTIVILAMOTYTRIFFICAROIDRINSSERANDRACDESSLET 255	

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GenCore version 5.1.6
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M protein - protein search, using sw model

August 5, 2004, 13:28:38; Search time 13 Seconds (withbor alignmenta) 1610.169 Million cell updates/sec no un

UG-10-018-257A-2 133 UNCLDANVSSEGFGSVEKV......BSQCHPPATSPLVAAQPSDT 402 itle: erfect score: equence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

141681 segs, 52070155 residues earched: otal number of hits satisfying chosen parameters:

141681

inimum DB seq length: 0 aximum DB seq length: 2000000000

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\*

atabase :

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homo sa	070528 cavia porce	P97288 mus musculu		Q29006 sus scrofa	P35406 carassius a				P21728 homo sapien			_	P07700 meleagris g	-	P53454 fugu rubrip	-	•		Q28044 bos taurus				P54833 canis famil		-	_	P97292 mus musculu			P18762 mus musculu		P34971 mus musculu
SUMMARIES	ΩI		5H4 CAVPO	SH4_MOUSE	5H4_RAT	SH4_PIG	DIDR CARAU	DIDR FUGRU	DADR XENLA	DADR DIDMA	DADR HUMAN	DADR PIG	DCDR_XENLA	DADR MACMU	BIAR MELGA	DIDR OREMO	DSDR_FUGRU	B2AR MESAU	DADR_MOUSE	DBDR_HUMAN	B2AR BOVIN	DADR RAT	DBDR_RAT	DBDR_XENLA	B2AR CANFA	HH2R RAT	B2AR MACMU	BLAR SHEEP	HH2R MOUSE	BIAR BOVIN	BIAR XENLA	B2AR MOUSE	BLAR RAT	B1AR_MOUSE
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	Query	95.7	91.6	89.7	88.4	30.4	28.6	27.7	27.6	27.5	27.3	27.3	27.2	27.2	26.9	26.9	26.6	26.5	26.5	26.4	26.4	26.4	26.4	26.3	26.2	26.2	26.1	26.0	25.9	25.9	25.9	25.8	25.8	25.7
	Score	2042	1954	1913	1886	648	610	591.5	588.5	587	582.5	581.5	280	579.5	574	573.5	268	266	564.5	563.5	562.5	562.5	562.5	562	559.5	559	256	554	553	553	551.5	550	550	549
	esult No.	7	6	М	4	Ŋ	9	7	æ	on.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

			sus scrofa felis silve mus musculu meleagris g
0923y9 0923y7	P07550 Q8hz64 P25021	P60021 Q28998 Q16950	Q28997 Q918t5 Q923y8 P43141
TAR1 RAT	B2AR_HUMAN TAR1_MACMU HH2R_HUMAN	HH2R PANTR B1AR PIG 5HT1 APLCA	B2AR_FIG B2AR_FELCA TARI_MOUSE B4AR_MELGA
44			
332	413 336 359	35.4 4 68 8 83	332 332 428 332
25.7	25.6 25.6 25.6	25.6 25.6 25.6	25.5 25.3 25.3
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TISONE SECURIOTI: Isoform 5-FTM(A) is expressed in ileum, brain,
and artium, but not in the Ventricle.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                  MEDIATES-2019:799; PROMEDGE-76559; MINDERT H.)
ESPITESED OF GENERAL MAINDAIN H.O., Lubbert H.)
ESPITESED OF GENERALINI SCREPTOR MENNAS IN blood vessels.";
ESPITESED OF GENERALINI SCREPTOR MENNAS IN blood vessels.";
-I- FUNCTION: This is one of the several different receptors for 5-
-I- FUNCTION: This is one of the several different receptors for 5-
-I- FUNCTION: This is one of the several different receptor that functions as a neurocranamister, a homome, and a mittogen The activity of this receptor is mediated by G proteins that Estmilates adendative
                                   PREDIREZ-GIOIGHIS PROMEGLIOCGGGG 1, Zhang Y.B., Gommeren W., Verbassel. P., Jurzah W., Ven Oers I., Zhang Y.B., Gommeren W., Verbassel. P., Jurzah W., Leyen J., Luyron W., Verbassel. P. Jurzah M., Leyen J. Luyron W., Verbassel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        •
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GO GO 10004991, Presercoint receptor activity; TAS.
GO, GO 10009191, PrG-protein signaling, coupled to cyclic nucl.
InterPro. IPRO00276; GPCR_Rhodpan.
                                                                                                                                                                                                                                                                                                                                                                                                             SÜBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing, Named isoforms=7;
Comment=Additional isoforms seem to exist;
Name=5-HT4(B);
                   OF 10-388 FROM N.A. (ISOFORM 5-HT4(F))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=013639-1; Sequence=Displayed;
Name=5-HT4(A); Synonyms=5-HT4S;
IsoId=013639-2; Sequence=VSP_001849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=5-HT4(D);
IsoId=013639-4; Sequence=VSP 001847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=S-HT4(B);
Synonyms=HH-HT4(g);
Isold=0,14639-5; Sequence=VSP_001846;
Name=S-HT4(F);
Isold=0,13639-6; Sequence=VSP_001845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=5-HT4(C);
IsoId=Q13639-3; Sequence=VSP_001848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELLY (1925 OF CANTAGE) | PRELLY ANTAGES OF CANTAGES OT CANTAGES OF CANTAG
                                                                                                                                           Neurochem. 74:478-489 (2000)
                                                                                                                                                                                 SEQUENCE OF 112-255 FROM N.A.
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                                                                                                                    novel 5-HT4 splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=5-HT4 (G);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 602164;
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                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 ---IEKRKFNQNSNSTYCVFMVNKPYAIICSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP_001847.
DAVECGGWESQCHPPATSPLVAAQPSDT -> F (in
                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
S-palmitoyl cysteine (By similarity)
PROSITE, PSO1237, G PROTEIN RECRP F.1.; 1.
PROSITE; PSS0262 G PROTEIN RECRP F.1.; 1.
G-procein compled tecepror; Transmembrane; Olycoprotein,
Malligene family; Lipoprotein; Paniarene Alexantaive splicing.
DOMAIN.
                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform 5-HT4(C)).
PTId=VSP 0018HS.
DATEGGOWESCHPPATSPLVAAQPSDT -> HQELEKLPIHNDPBSLESCF (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                   -> LERSLNOGLGODFHA (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2042; DB 1; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 001849.
Missing (In isoform 5-HT4(G))
/FTId=VSP 001850.
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                                                                                                       CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7FCFEC60E7BDP560 CRC64;
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388

STITINGSTHVLRDAVECGGOWESQCHPPATSPLVAAQPSDT

347

Pfam; PF00001; 7tm 1; 1. PRINTS; PR00237; GPCRRHODOPSN.

120 169 240

9 9

14; Gaps

Indels

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241 QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 ---IBKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHARQI 226
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                                                                                                               61 SLAPADLIVSVLVMPFGAIELVQDIMVYGEMFCLVRTSLDVLLTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                           121 AICCOPLVYRNXMTPLRIALMIGGCWVIPMFISFLPIMQGWNNIGIVDL------
                                                                             1 MDKLDANVSSEBGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDROLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                          FHAIEKRKFNONSNSTYCVFMVNKPYALTCSVVAFYIPFLLMVLAYYRIYVTAKBHAHQI
                         10;
92.0%; Pred. No. 3.5e-136;
tive 8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 5-HT4 (F)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ann. N.Y. Acad. Sci. 861:49-56(1998).
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                              Conservative
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Best Local Similarity
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                              Matches 370;
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5H4_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISs-PROTENTY is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMED outstation the Burgoem Bioinformatics Institute. There are no restrictions on its use by non-pipe statisticitions as long as its content. Is in no way modified and this exterment is not removed. Usage by and for commercial entities a Ticense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as a neuroiransmitter, a hormone, and a mitogen, The activity of
this receptor is mediated by G proteins that stimulates ademylate
S/GBCELUARA (LOCYTOR: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van den Wyngaert I., Gommeren W., Jurzak M., Verhasselt P., Gordon R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variants",
Submitted (UNI-1997) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: This is one of the several different receptors for 5-
-- FUNCTION: This is one of the several different bank functions
hydroxytryptamine (sertocoin), a biogramic hormone. The activity of
                                                                                                                                                                                    (Rel. 39, Last sequence update)
(Rel. 42, Last amnotation update)
admine 4 receptor (5-HT-4) (Serotomin receptor) (5-HT4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=070528-1, Sequence=Displayed;
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                               Gavia porcellus (Guinea pig).
Bukaryotar Netazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Memmalia, Butheria, Robentia, Hystricognathi; Gaviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interfect of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leysen J., Luyten W., Bender E.; "Cloning and expression of 5-HT4 receptor species and splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL) .
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D45B3A37F60D02B CRC64;
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1 (POTENTIAL).
------ (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced;
                                                                                                           388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL)
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                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR000276, GPCR_Rhodpsn.
                                                                                                                                                                                                                                           5-hydroxytryptamine 4 receptor
                                                                                                                                                              (Rel. 39, Created)
(Rel. 39, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y13585; CAA73912.1; -. HSSP; P29274; IMMH.
                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=10141,
                                                                                                                                                              30-MAY-2000
                                                                                                                                                                                        30-MAY-2000
                                                                                                      5H4 CAVPO
070528;
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                                                   ESULT 2
H4_CAVPO
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584 WOLES GYRNDADD, PRT, 388 AA.
15-701-386 (095004, 095004, 095244;
15-701-399 (Rel. 36, Created)
15-701-399 (Rel. 36, Last americancion update)
15-007-300 (Rel. 42, Last americancion update)
15-007-300 (Rel. 42, Last americancion update)
15-007-300 (Rel. 42, Last americancion update)
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Claeyen S., Faye P., Sebben M., Taviaux S., Bockaert J., Dumuis A.;
S-HY4 receptors: cloning and expression of new splice variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euceleostomi, Memmalia, Eucherida, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGORNACE ROOM NA.
STRANLBOWISSE TISSUE-Beals;
STRANLBOWISSE TO TO TO THE PROBLESSES,
CLASVER 5, Sebben M., Johnnot L., Bockaert J., Dummis A., Clanyen 5, Sebben M., Johnnot L., Bockaert B., Sebben M., Johnnot L., Bockaert J., Dummis S., Teceptor, T., Te
STITLINGSTHVLRDAVECGGQWESQCHPPATSPLVAAQPSDT 402
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                                                                                                  STTTINGSTHVLRDTVECGGQWESQCHPAASSPLVAAQPIDT 388
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STRAIN=Swiss; TISSUE=Brain,
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91.6%; Score 1954; DB 1; Length 388;

Query Match

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120
                                                                                                                                                                                                                                                                      121 AICCOPLVYRNKWTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
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MEDLINE-Sig19s, PAMAGH-102020.

MORAL Inchi-specific S-HTW receptor splice variants show marked bloom their-specific S-HTW receptor splice variants show marked constitution activities roll of the Creeminal intracellular domain."; Mon Planmaco. 18:110-920(1999).

FORTIONS THE SIG10-920(1999).

PAMAGHORY TOPPER SIGNOR THE SECOND TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---IEKRKFSHNSNSTWCVFWVNKPYAITCSVVAFYIPPLLMVLAYYRIYVTAKEHAQQI
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01-0758, 08034, 082757, 08306;
01-070-1397 (Rel. 13; Lat at antendence update)
11-070-1307 (Rel. 13; Lat at antendention update)
11-070-1307 (Rel. 13; Lat at antendention update)
11-070-1307 (Rel. 14; Lat at antendention update)
11-070-1307 (Rel. 14; Teogrotor (S-HT-4) (Serotonin receptor) (S-HT4)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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"Expression of servoronin receptor mRNAs in blood vessels.";
FRBS Lett. 370:215-221(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
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DVBGOOPSRCHIANSPLWADOPVIRRPONDIEDSC
(In 16809 - YTTLARGONGELENGTRENDESISSCE
(In 1680 - STRT48).
FYTLARGO SON 1854.
RUPYROGONGS4.
RUPYROGONGS4.
RUPYROGONGS58.
SIGNSS6. - SFPLLEVRRPYW (In 18070m EDBOC
                                                                                                                                                                                                                                                                                          Isold=66755-3; Sequence=VSP 001855;
TISSUS SPECIFICITY: In brain, the 5-HT4s transcripts are
restricted to the strictum, but the 5-HT4L transcripts are
expressed throughout the brain, except in the esreballum. In
periphera itsaues, differential expression is also observed in
the artium of the heart where only the 5-HT4S isoform is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Page | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-HT4(E)),
/FTId=VSP 001855.
NA -> MP (IN REF, 3).
A1889155A08930B4 CRC64;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                            Isold=Q62758-2; Sequence=VSP_001854;
Name=5-HT4(E);
                                                    Name=5-HT4L;
IsoId=Q62758-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 75 N
406 AA; 46107 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1447

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Onery March
Best Local Similarity 98,41; Score 1865, DB 1; Length 406;
Best Local Similarity 98,51; Fred No. 3.4-0.31;
Marches 16; Indels 14; Gaps 1

MORLDANVSSERGFGSVEKVYLIFLSTVILMALIGALLYMVAVCMORQLRKIKTNYFIV 60

MORLDANVSSKRÖCKSVVALAFFANTLANLIGALLYMVAVCMORQLRKIKTNYFIV 60

MORLDANVSSKRÖCKSVXVALAFFANTLANLIGALLYMVAVCMORQLRKIKTNYFIV 60

FT DOWALN   1 24 EXTRACELLILAR (POTENTIAL)   1 25 EXTRACELLILAR	Quary Machine   14,   1,   1,	RESULT 7  DIDR FUGNU  1D DIDR FUGNU  1D CATALOG
FT TOWNING 1 15 CCTTOBLASHIC (FOTENTIAL). FT TOWNING 1 16 36 4 (FOTENTIAL). FT TOWNING 1 15 10 5 (FOTENTIAL). FT TOWNING 1 17 10 1 10 1 1 1 1 1 1 1 1 1 1 1 1 1	0y 241 [CRACASSESREARCHETTCALK 273  Db 107 LGRACASCESREARCHETTCALK 137  BESULT 6  100 DIDE CARAU STANDARD, PRT, 363 AA.  P345 [CRACACT STANDARD, PRT, 363 AA.  P35 [CRACACT STANDARD, PRT, 364	

451 AA.

STANDARD;

DADR XENLA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 FGAIBLVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCOPLVYRNKATP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 WKAATEIMGFWPFGE-PCNIWVAFDIMCSTASILNLCVISVDRYWAI-SSPFRYERKMTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 LRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGODFHAIEKRKFNQNSNS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 TY------CVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TYAGDLPPDNCDSSLNRTYAISSSLISFYIPVALMIUTYTRIYRIAQKQIRRISALERAA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ASSESRPQ-----SADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAPFFVTNIVDFFI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 SSKRVLTGCFLSLLIFTTLLGNTLVCVAVTKFRHLRSKVTNFFVISLAISDLLVAILVMP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVEXVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLARADLLVSVLVMP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
   297 EADDITDFPCISSTIFDVFVWFGWANSLNPIIYAF-NADFRKAFSILLGC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DY-----TVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLILLCC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2.4e-36;
60; Mismatches 114; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.7%; Score 591.5; DB 1; Length 459;
                                                                                                                                                                                                                                                                                                                                   interFor, IFP000276, GPCR_Rhodpen.
Pfens. PP00001, 7tm 1, 1.7
PRINTS. PR00017, GECRHODOPSN.
PROSTER, P800037, GEOFFIN BRCRE. P. 1, 1.
PROSTER, P800037, GEOFFIN BRCRE. P. 1, 2, 1.
PROSTER, P800037, GEOFFIN RECEP. T. 2, 1.
Whiligene Samily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARIT
puffer fish Pugu rubripes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51080 MW;
                                                                                                                                                                                                                                                                                              EMBL; X80174; CAA56455.1; -. PIR; A56849; A56849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 37.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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TRANSMEM
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ESULT 8 ADR\_XENLA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDLLVAVLVMPWKAVAEIAGFWPFG-TFCNIWVAFDIMCSTASILNLCVISVDRYWAI- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 SMDEDVLLTERESSFRVLTGCFLSVLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVISLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVEKVVLLT------FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA
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                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.

SEQUENCE PROM N.A.

SEQUENCE - SECULIA SECULIA SECULIARIA SECULIA 
                                                                                                                                 Mentalia zecepta (African Clawed frog).

Bukarjula javi Metazoa (African Clawed frog).

Bukarjula Metazoa (African Clawed frog).

Ambrinjula Bartendia, Amura Mesobartachia, Pipoidea, Pipidee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 S-palmitoyl cysteine (By similarity) 50549 MW; 3A0F8AB36C166687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRODAZI; GECREMODORSN.
PRINTS; PRODAZI; GECREMODORSN.
PROSTITE, PSSOAZI; G. PROTEIN PRECEP F1 2; 1.
PROSTITE; PSSOAZI; G. PROTEIN PRECEP F1 2; 1.
G-protein coupled réceptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene family, Lipoprotein, Palmitate.

1 22 EXTRACELULAR (POTENTIAL).
TRANSEM 23 48 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.6%; Score 588.5; DB 1
34.5%; Pred. No. 3.8e-36;
                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U07863, AAAS0828.1; -.
PIR, ISLSES9, ISL6S9.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1, 1.
                                                                                                                                                                                                                                            Xenopodinae, Xenopus.
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NA CARL	OX NCI_TAXID=5606; RN NCI_TAXID=5606; RN IND_TAXID=5606; RN EXPLINE-97039; PubMed=2144334; RX MEDLINE-9710093; PubMed=2144334; RX Dearry A., Gingrich J.A., Falardeau P., Fremeau R.T. Jr., Bates M.D., RX TWO.Scollar cloning and expression of the gene for a human D1 dopamine RT Treeppor. RT TREEPPORT RT RT RESPONSE RT RT RESPONSE RT RT RESPONSE RT
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us-10-018-257a-2.rsp

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MEDLINE-90370094; PubMed-2168520; Xushner J.A., van Tol H.H.W., Zhou Q. -Y., Grandy D.K., Thabbi L., Xushner J.A., van Tol H.H.W., cone R., Pribow D., Salon J., Bursow J.R., Civelili O.; "Cloning and expression of human and rat DI dopamine receptors.";
                                                                                                                                                                                                                   Nature 347:76-80(1990).
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Surablara R.K., Mignik H.B., Weiner D.M., Stormann T.M., Brann M.R., Skennedy J. W., Glennether J.S., Glennether J.S., Rozmahel R., Yang Y., Israel Y., Skennedy O. Dowd B.F., Shannan Department of the State of the

Nature 347:80-83(1990).

Ohara K., Ulpian C., Seeman P., Sunahara R.K., van Tol H.H.M., Niznik H.B.; MEDLINE=93228762; PubMed=8471124; SEQUENCE PROM N.A. TISSUE-Brain;

"Schizophrenia: dopamine D1 receptor sequence is normal, but has DNA polymorphisms."; Neuropsychopharmacology 8:131-135(1993)

[15]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEVENT TO COUCHI I., Arita M., Putami K., Mateumoto S.,
Suva M., Sato T., Okouchi I., Asii K., Akiyama Y., Ir.
Testemum S., Aburatami H., Assi K., Akiyama V., Ir.
Testemum S., Aburatami H., Assi K., Akiyama neven transmembrane holix
"Genome wide."

SEQUENCE FROM N.A. TISSUE=Brain;

Puhl H.L. III, Ikeda S.R., Aronatam R.S.; "CDMA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; Submitted (APR-2002) to the EMBL/Genbank/DDBA databases.

PALMITOYLATION OF CYS-347 AND CYS-351.

MEDLINE-2008665; pubMed-1061869;
"Palmicroll H. Xide 2. George 8. R., O'Dond B. P.;
"Palmicroll H. Xide 2. George 8. R., O'Dond B. P.;
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EMBL; X55758; CAA39284.1; -EMBL; X5570; CAA39286.1; -EMBL; X5897; CAA41734.1; -EMBL; SS841; AAB253.1; -EMBL; AB05677; BAC05902.1; -EMBL; AR99861; AAM18131.1; --PIR; S11377; DYHUD1. Genew, HGNC:3020; DRD1.

1,12643). C.cell; TAS.

GO:0005623; C.cell; TAS.

GO:000587; Cithegral to plasma membrane; TAS.

GO:000587; Edopamine receptor activity; TAS.

GO:0007027; Fidopamine receptor activity; TAS.

GO:000727; Pidopamine receptor signaling pathway; TAS.

6 [POTENTIAL].

\*\*REACELLULAR (POTENTIAL).

\*\*POTENTIAL).

CTODELASHIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

BY SIMILARITY. Ouery Match

27.3%; Score 582.5; DB 1; Length 446;
Best Local Similarity 33.7%; Pred. No. 18-35;
Matches 139; Conservative 67; Mismatches 139; Indels 71. 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) 64E062D765D0DBA7 CRC64; /FIId=VAR 014671. R -> S (in dbSNP:5330). /FIId=VAR 014672. S -> A (in dbSNP:5331). S-palmitoyl cysteine. S-palmitoyl cysteine. T -> P (in dbSNP:5327). -> R (in dbsNP:5328). FTIG=VAR 014670 /FTId=VAR 014673 49293 MM; 199 347 37 446 AA; 313 338 347 351 37 37 199 DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM CARBOHYD FRANSMEM FRANSMEM SECUENCE CONFLICT VARIANT **TARIANT** /ARIANT MRIANT DOMAIN DOMAIN LIPID CIPID 

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GCFCLCWAPFFVTNIVDPFI-----DYTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSF 279 GVFVCCWLPFFILNCILPFCGSGETOPFCIDSNTFDVFVWFGWANSSLNPIIYAF-NADF 280

Thu Aug

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                            65 SLAVSDLLVAVLVMPWKAVAEIAGFWPFGS-FCNIWVAFDIMCSTASILNLCVISVDRYW 123
SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                                                                                                                                                                                                                                                  241 OMLORAGASSE-----SRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCW 286
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                                                                                                                                                                                                                                                                                                                                                                                                                         287 APFPUTNIVDPFI-----DYTVPGQVWTAPLMLGYINSGLNPFLYAFLNKSFRRAFLII 340
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                                                                                                                                                                                                              19. FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                           183 TH--------NCDSSLSRTYAISSSLISFYIPVAIMIVTYTRIYRIAOKOIRRI
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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92
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Grenader X.C. () Yearner D.A. Healy D.P.;

By Chill G. Pit C. Pit C. H. S. () Adopanie receptor gene expressed in renal Application of the portraine D.A. dopanie receptor general L.C. Pit C. 11. () Add (1995).

-I - FINCTION: This is one of the five types (DI to D5) of receptors procedure. The activity of this receptor is mediated by G procedure which activate ademyly Cycles of the processor of the STRINGTY: Interacts with calcyon (by similarity).

-I STRINGTY: ABLONGS to Camily J. Of Grorein coupled receptors.
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Mammalia; Eurheria; Cetartiodactyla; Suina; Suidae; Sus.
NCRI_TRATID=9823;
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S-palmitoyl cysteine (By similarity)
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N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                       (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
                                                         446 AA.
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                                                         STANDARD:
                                                                                                                                                                                          D(1A) dopamine receptor.
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                                                                                                                                                                                                                                           Sus scrofa (Pig)
                                                                                                           01-OCT-1996
01-OCT-1996
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SEQUENCE
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    RESULT 11
DADR PIG
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	7,	94	145	205	262	311	
43 CYTOPLASHIC (POTENTIAL). 43 CYTOPLASHIC (POTENTIAL). 53 EXTRACELLULAR (POTENTIAL). 54 CYTOPLASHIC (POTENTIAL). 54 CYTOPLASHIC (POTENTIAL). 55 CYTOPLASHIC (POTENTIAL). 56 CYTOPLASHIC (POTENTIAL). 56 CYTOPLASHIC (POTENTIAL). 57 CYTOPLASHIC (POTENTIAL). 58 CYTOPLASHIC (POTENTIAL). 58 N-LINEED (GLONC) (POTENTIAL). 59 P SIMILARIY. 50 PATHABOLOL (POTENTIAL). 50 PATHABOLOL (POTENTIAL). 51 PATHABOLOL (POTENTIAL). 526.0 MW, FAIRBED (GLONC) (POTENTIAL). 526.0 MW, FAIRBED (GLONC) (POTENTIAL).	27.2%; Score 580; DB 1; Length 465; 39.0%; Pred. No. 1.7e-35; ive 53; Mismatchee 114; Indels 36; Gaps	LSTVILAAILGRILIMWAVCWDROLRKIKNYPIVSLARADILVSVLWAPROAIELVODI 6 	AIYGEVPCLVRTSLDVLLTASIFHLCCISLDRYAAICCQPLVYRNKMFPLRIAMLGCC 1 	WVIPTEISFLPIMOGWNNIGIIDLERSLMOGLOGOPHAIERGRENONSNSTYCVFWVME :   IIIII    naitcswapyipplamvaayriivvakehaholohloragassesrpgadohst ;    :  :       :	HEMETETRAAKTLCIIMGCECLMAPEVTNIVDPPIDTYPDGO	LNIGTINSGINPPINAFINKSPRARELILICCD 344	
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(Rel. 40, Created) (Rel. 40, Last sequence update) (Rel. 42, Last annotation update) 446 AA STANDARD; 16-OCT-2001 ( 16-OCT-2001 ( 10-OCT-2003 ( DADR MACMU 077680; ESULT 13 ADR MACMU

D(13) dopamaino receptor.

D(13) dopamaino receptor.

Mocaca malatta (Rhesus macaque)

Sukaryors Meracao; Chordera; Craniata; Verrebrata; Eureleostomi;

Mammalia Eurhesia; Primaces; Cararrhini; Cercopithecidos;

Cercopithecines Macaca.

receptor gene.\*;
Pharmacol. 4::62-659(1992). The five types (DI to D5) of receptors Pharmacol. A::62-659(1992). The five types (DI to D5) of receptors for doparamen. The activity of this receptor is mediated by G proteins which octivate adentyly cycles are protein. Support of the control is a support of the control in the calcyon (by similarity).

- SUBDATY. PROTEINER DESCRIPE THE CALCON. THE SUPPORT OF "Molecular cloning and expression of the rhesus macaque D1 dopamine SEQUENCE FRON N.A. PRODINES-92235540; PubMed=1533268; Machida C.A., Searles R.P., Nipper V., Brown J.A., Kozell L.B., Neve K.A.;

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CYTOPLASNIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY. | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | Real | 49292 MW; 351 3 446 AA; CARBOHYD LIPID

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This GWISG-ROOT entry is copyright. It is produced through a collaboration between the Swise Institute of Boinformatics and the EMES contextion the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EMES of the EM
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                                                                                                                                                                                                                48 MALVVLLIVAGNVLVIAAIGREQRLQTL-TNLPITSLACADLVMGLLVVPFGATLVVRGT
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FUNCTION: This is one of the five types (DI to DS) of receptors for department of this receptor is mediated by G proceins which activate ademyly cyclase.

-: SURCIMICAN LONGWING Integral membrane procein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Crainiata, Vertebrata, Butaleostcomi;
strinopterygii, Meopterygii, Teleostei, Buteleostei, Roteleostei, Asanthomorphia, Asanthopterygii, Percomorphia, Perciformes, Labroidek;
Asanthomorphia, Asanthopterygii, Percomorphia, Perciformes, Labroidek;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D(1)-like dopamine receptor.
Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica)
                                                            Length 483;
                                                                                                                        57; Mismatches 135; Indele
483 AA; 54078 MW; B11A7E71F6CCE3E4 CRC64;
                                                            26.9%; Score 574; DB 1;
37.0%; Pred. No. 4.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                        Watches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cichlidae, Oreochromis.
                                                                                        Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPH: Homologous desensitization of the receptor is mediated by its phosphorylation by beta-adrenergic receptor Kinsse. SIMILARIF: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINES-519665, PROMED-1882019.

18. Mindabaer R., Palm D., Schmackerz K.D.; Epptidae derived from H. Windabaer R., Palm D., Schmackerz K.D.; Epptidae derived from the third intracellular loop of the beta-adrenoceptor."; PERS Lett. 389.133-136.1395).

1. FOUCTION: BESTA-ADREMENTOR RECEPTORS MEDDATE THE CATECHOLMINE-INDUCED ACTIVATION OF G. SPECTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'The avian beta-adrenergic receptor: primary structure and membrane
                                                                                                                                                    Meleagris galloavo (Comon turkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauris, Nees, Neognathae, Galliformes, Phasianidae, Meleagris,
(NELTAXID-910);
                                                                                                                                                                                                                                                                                                                                                      WEDLINE=66313664; PubMedd=3018746;
Varden Y., Rodriguez H., Wong S.K.-F., Brandt D.R., May D.C.,
Burniez J., Harkins R.N., Chen E.Y., Ramachandran J., Ullrich A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-palmitoyl cysteine (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ppBB; IDER; 14-607-19;
III.eEFPC; IFR000276; GPCR_Rhodpen.
Pfam., PF00011, Tm. 1.1.
PF00217; PS000217; GPCRRHODOPSN.
PF002179; PS000317; GPCRRHODOPSN.
PF002179; PS000317; GPCRTEN RECEP_F1_1; 1.
PF002179; PS000404; GPCRTEN RECEP_F1_2; 1.
GP. PF00416; GPCRTEN RECEP_F1_2; 1.
RALFIGURE Amily; Phosphory/ation; Lipoprocein; Palmitato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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Proc. Natl. Acad. Sci. U.S.A. 83:6795-6799(1986).
                                                       01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Beta-1 adrenergic receptor (Beta-T).
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26.9%; Score 573.5; DB 1; Length 386;
Ilarity 38.2%; Pred. No. 4.28-35;
Conservative 51; Mismatches 119; Indels 37; Gaps
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Best Local Similarity Matches 128; Conserv

265 -MRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFIDY----TVPGQVWTAFLWLGYI 317

completed: August 5, 2004, 13:34:49 earch completed: A

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1 090X37	1 090282	1 Q8BLD9	1 Q8VHQ5	3 042317	3 Q9YHA5	1 Q9CRR2	1 Q8BH38	3 042318	1 Q923Y9	98178G	QBHZG3	Q8HZG2	1 Q923Y7	Q96EC3	Q8HZ64	OSHZG0	Q725R9	OBNEO9	1 Q923Y8	1 Q8VBU7	Q8HZG1	Q96RJ0	3 Q7T077	Q86ME5	Q9VFM1	Q24038	Q86ME4	1 Q99P04	
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Pintal, 6669; 186495; 186495; 186409; 1884.

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NCSI.TRATE:9823;
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MEDLINES-5365798; bubbeds.7656980;
Ullner C., Schmack K., Kalkman H.O., Lubbert H.,
Expression of serotonin receptor mRNAs in blood vessels.";
PERS Lett. 730.215.521(1995).
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151 AA; 17240 MW; 6505B7CB46328750 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Lest sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Serotonin 4A receptor (5-HT4A) (Fragment).
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T. "Submitted (SEP-2000) to the BMEL/GENBRAK/DED4 databases
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T. SIMILARITY: BELOWGS TO FAMILY 10° G-RACTERIN COUPLED RECEPTORS.
T. SIMILARITY: BELOWGS TO FAMILY 10° G-RACTERIN COUPLED RECEPTORS.
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Mamnalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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88.1%; Score 1879; DB 4; Length 387;
Best Local Similarity 95.7%; Pred. No. 4.5e-72;
Matches 360; Conservative 0; Mismatches 2; Indels 14
                                                                   0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DEC-2003 (TrEMBLrel. 24, Last annocation update)
         96.3%; Pred. No. 1.3e-190;
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                                                                   1; Mismatches
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                                                                   387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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         Best Local Similarity
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Q96KI0
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289 FFVTNIVDPFID-----YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLII- 340

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60 VSIAFADLLVSVLVMPFGAIELVQDIMIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRY 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 YAICCOPLVYRNIONTPLRIALMIGGCWVIPTFISFLPIMGGWNNIGIIDLERSLNQGLGQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 DFHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTA---- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 TLKVMAERPDD------CLFIVNKAYAVVSSSISFWIPCTIMVFVYLKIYMEARRQEKQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KEHAHQIQMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIINGCFCLCWAPFF-- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 IKQSGYHIKELSPSEQTNLTDDQSENRNERKRNRREHKAAKTLGIIMGAFVFCFLPFFTW 295
                                      219 FFVLNCMVPFCNPNGGSDFFCISSTTFDVFVWFGWANSSLNPIIYAF-NAGFRKAFSILL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LDANVSSEEGFGSVEKVVLLTFLSTVILM----AILGNLLVMVAVCWDRQLRKIKTNYFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VINIVDPFIDYTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIIL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petetive G. protein oxopled receptor.

Bikanda solidisasima (Allantic surf-clam).

Bikanyota, Mestaoya, Mollucca, Bivalivia; Heteroconchia; Veneroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 AA; 44383 MW; C65E8AF910447347 CRC64;
                                                                                                                                                               341 ----LCCDDERYRRPSILGOTVPCSTTTINGSTHVLRD 374
                                                                                                                                                                                                                                           338 GCHRLCPGSNAIEIVSİNNNGGPPSTSQYQPKGHVPKE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annocation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 SSPFRYERKMTPKVAPIMISLAWTLSILIŚFIPVQLNWH----------- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 IEKRKFNONSNSTY-----CVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEH 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 ----KAQABLMGTYGELPPDNCDSSINRTYAISSSLISFYIPVAIMLYTYTRIYRIAQKQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 AHQIQMLQRAGASSESRPQ----SADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 IRRISALERAAESAKNRHSSMGNNASMESESSFKNSFKRETKVLKTLSVIMGVFVCCMLP 278
                                                                                                                        AIEKRKFNONSNSTYCVFMVNKPYAITCSVVAPYIPPLLMVLAYYRIYVTAKEHAHOIOM 242
                                                                                                                                                                           61 VIEKRKFHQNSNSTYCIFMYNKPYAITCSVVAFYIPFLLMVLAYWRIYYTAKEHAHQIQM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PADLLVSVLVMPPGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA 63
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinus carpio (Gomon carp).
Bakaryota Metazoa, Chordata; Craniata; Vertebrata; Eutaleostomi;
Bakaryota Mesoperygii; Neopterygii; Neopterygii; Ostariophysi; Cyprinus
Cyprindes; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
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28.1%; Score 599; DB 13; Length 43
Bert Local Similarity 35.7%; Pred. No. 6.28-50;
Marches 142; Conservative 63; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    243 LORAGASSESRPOSADOHSTHRMRTETKAAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D1A4 dopamine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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N ANDINE-9594415; Phybele-950515,
HICTORO J. ACCIDET S.N. Disappor M. B. A.;
HICTORO J. ACCIDET S.N. Disappor M. B. A.;
HICTORO J. ACCIDET S.N. Disappor M. B. A.;
HICTORO J. ACCIDET S.N. Disappor M. B. A.;
Trechines: clouding, sequencing and comparison of five D1-like and three in D2-like receptors.
Bracept. Channels 5:187-40 (1998).
C. I. SUNCELLULAR LOCATION: HINSTEAL MEMBRANE PROTEIN (BY SIMILARITY).
C. I. SUNCELLULAR LOCATION: HINSTEAL MEMBRANE PROTEIN (CUPLED RECEPTORS. M. CO.) OLIO 1018-12; Freceptor activity, IRA.
R. GO; GO: 0001594; Freceptor activity, IRA.
R. GO; GO: 0001594; Freceptor activity, IRA.
R. GO; GO: 0001512; Freceptor activity, IRA.
R. GO; GO: 0001517; Freceptor activity, IRA.
R. R. GO; GO: 0001517; Proceptor activity, IRA.
R. R. R. France Processes of GRR Rhodpen.
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           94 STDDADGSSHLALVFVKCFIIGFIILAAILGNMLVIVSVMRHRKLR-IITNYFVVSLAVA 152
                                                                                           126 PLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIB 185
                                                                                                                                                                                          212 PLDYPLIMIQRRVFIMILMVWLSPALLSFLPICSGW-------YTTTE 252
                                                                                                                                                                                                                                                             186 KRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQR 245
                                                                                                                                                                                                                                                                                         246 AGASS------ESRPO-SADQHSTHRMRIETKAAKTLCIIMGCFCLCWAPFFV 291
                                                                                                                                                                                                                                                                                                                                                                                            64 FADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIPHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                       DLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIPHLCCISLDRYYAICCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eŭkaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 INIVDPFIDYTVPGQVWTAFL-WLGYINSGLNPFLYAFLNKSFRRAF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 WYIVSSLCDSCITPRLLVGILFWIGYFNSALNPIIYAYFNRDFRAAF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%; Score 593; DB 13; Length 446; 34.5%; Pred. No. 2.5e-49; ive 68; Mismatches 138; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in Mirs; PRO0317 GPGRHODOPSN.
PROSTIFF; PRO0317 GPGRHODOPSN.
PROSTIFF; PRO0317 G. FROTEIN RECRE F1_1; 1.
G-proce and Company of PROSTIN RECREP F1_2; 1.
G-proce and complete Receptor; Transmembrane.
G-proce and complete Receptor; Transmembrane.
SEGURNE 445 AA, 45800 MM; 41783430352730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1343 dopamine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel, 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%;
Ouery Match
Best Local Similarity 34.5%;
Matches 142; Conservative
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NCBI TaxID=7962;
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                                                                                                                                                                                                                                                                                                                     And Administration to Children St. F. Holt R.A., Byans C.A., Occayne J.D., By Manner M.D., Children St. F. Holt R.A., Byans C.A., Occayne J.D., R. Manner M.D., Children St. F. Holt R.A., Byans C.A., Chen L.A. M. St. M. Children St. F. Stitton G. G., Wortran J. R., Yordell M.D., Thango G. M. Chen L.A. By Stitton G. G., Wortran J. R., Yordell M.D., Thango G. M., Chen L.A. Bar A. M. A. M. Oyle C., Barter E.G., Helt G. Neilenc C.R., Mikios G.L.G. Bar M. K.H., Doyle C., Barter E.G., Helt G. Neilenc C.R., Mikios G.L.G., Barler B.C., Barler B.D., Branch J. B. Barter E.G., Helt G. Neilenc C.R., Mikios G.L.G., Barler B.C., Barler B.D., Branch J. B. Barter B.C., Barler B.D., Branch J. B. Barter B.C., Barler B.D., Branch J. B. Barter B.C., Barler B.D., Branch J. B. Barler B.C., Barler B.D., Branch J. B. Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Barler B.C., Goog F. Congrey D. Helman J.J., Helmander J. M. Britis M.C., Barler B.C., Goog F. Congrey D. Helman J.J., Helmander J.M., Mchand M.C., Barler B.C., Ba
                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.1%; Score 598.5; DB 5; Length 508;
                                                                                                                                                      Neoprera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBL TaxID=7227,
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8.2e-50;
                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 138; Conservative
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                       CG6919 protein.
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12;

54; Mismatches 112; Indels 43; Gaps

Db   66 V8DL/VAILWHPKAVTEVAGWPEGS-PCNIMVACDIMCSTASILALCIISVDRWAAI-123	RESULT 9  OBMACA PRELIMINARY, PRT, 418 AA.  OBMACA PRELIMINARY, PRT, 418 AA.  OBMACA PRELIMINARY, PRT, 418 AA.  OBMACA PRELIMINARY, PRT, 418 AA.  OBMACA PRELIMINARY, PRT, 418 AA.  OBMACA PRELIMINARY, PRT, 418 AA.  OBMACA PROPERTY CONTROL OF THE SHORT PRELIMINARY PRELIMINARY PRESENCE OF THE SHORT PROPERTY OF THE SHORT PROPERTY	67 65 ADLAVSVLAMPPGALELVQDIALYGEVPCLVRTSLDVLATTAGFRELCCISLDRYALICC 124
124 SSPRIERENTPUAPIMISTALISTIVOLINI———————————————————————————————————	SENTY 8  OBSERT, 9  OBSERT, 9  OBSERT, 9  OBSERT, 9  OF TERELMINARY, PRT; 445 AA.  OBSERT, 9  OF TERELMINARY, PRT; 445 AA.  OBSERT, 9  OF TERELMINARY, PRT; 445 AA.  OF TERELS, 02, Last sequence update)  OL-TWR-1997 (TERELMINE, 02, Last sequence update)  OL-TWR-7003 (TERELMINE, 02, Last sequence update)  OL-TWR-7003 (TERELMINE, 02, Last sequence update)  DODAMINE DATE TEREPORT.  AND THE SECOND CONTROL OF TEREPORT SECOND CON	8 E E

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61 SLAFADLLVSVLVMPFGALELVQDIWIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRXY 120
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241 OMLORAGASSESR----PQSADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAPFFVTNI 294
                                                                                                                 228 SALERAAESAKONRHSSMGNSIESSSSPKMSFKRETKVLKTLSVIMGVFVCCWLPFFILNC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 SLAVSDLLVAVLVMPWKAVAEIAGFWPFGS-PCNIWVAFDIMCSTASILNLCVISVDRYW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AICCOPLYYRNKWIPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AI-SSPRYERKMIPKAAFILISVAWILSVLISFIPVOLSWHKAKPTGPSEGNATSLGKT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 OMLORAGASSE-----SRPOSADOHSTHRWRIETKAAKTLCIIMGCFCLCW 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 NTSTMEGTGLVAERDFSFRILTACFLSLLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVI 64
                                                                                                                                                               295 VDPFIDYT------VPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRAFLIILCC 343
                                                                                                                                                                                        288 MVPFCEQAPQGAADLPCVSSTTFDVFVWFGWANSLNPIIYAF-NADFRKAFSTLLGC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 NVSSEGFGSVE-----KVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FHAIBKRKFNQNSNSTYCVFMVNKPYAITCSVVAPYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Biteleostomi, Memmila, Butheria, Gesartiodactyla, Ruminantia, Pecora, Bovoidea, Bovinae, Bos. M. Pecora, Bovoidea, Mexima Fos. M. Pecora, Bovoidea, Pecora Meria Fos. M. Pecora, Pecora Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meria Meri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Mismatches 138; Indels
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PROSTITE, PRO0317, GFGTEN REXP. F1 j. 1.
PROSTITE, PROSTIS, GFROTEIN REXP. F1 2; 1.
G-PROSTIS, PROSTIS, RECEPCT, TATABREMENIE.
G-PROSTIS, CHARDEN RECEPCT, TATABREMENIE.
                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.2%; Score 580; DB 6;
34.4%; Pred. No. 4.6e-48;
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                                                                                                                                                                                                                                                                                                                            446
                                                                                                                                                                                                                                                                                                                        PRT;
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Matches 135; Conservative 6
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Dopamine 1A receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                      CBWND7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 EKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQ 244
                               235 RSEGREHTONLSQVEQDGRSGHGLRRSSKFYLKEHKALKTLGIIMGTFTLCWLPFFIVNI 294
                                                                                                                                                                                                                 295 VHVIQDNLIPKEVYILLMWVGYVNSAFNPLIYC-RSPDPRIAFQELLC----LRRSALK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 COPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMGGWNN---IGIIDLERSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAGASSESRPQS---ADQHSTHRMR-----TETKAAKTLCIIMGCFCLCWAPFFVTNI 294
                                                                                                                                                                                        295 VDPFIDYTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSIL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 FADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 FHAIBKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LDGDLPEKD---SSARVLTGCFLSLLILTTLLGNTLVCAAVTRFRHLRSKVTNFFVISLA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Early emergence of three dopamine DI receptor subtypes in
vertebrates. Molecular phylogenetic, pharmacological, and functional
criteria defining DIA, DIB, and DIC receptors in European eel Anguilla
anguilla";
                                                                                                                                                                                                                                                                                 35 GQTVPCSTTTINGSTHVLRDAVEC--GGGWESQ--CH-PPATSPLVAAQ---PSDT 402
                                                                                                                                                                                                                                                                                                                            349 AYGNDĆSSNS-NGKTDYTGZPNVCHQĞQEKERELLCEDPPGTEDLVSCPGTVPSDS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97160583; PubMed=9006917;
Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anguilla anguilla (European freshwater eel).
                                                                                                                                                                                                                                                                                                                                                                                                                                             445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dopamine DIA1 receptor.
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286 LPFFILNCMVPFCGSGETKPFCIDSITFDVFVWFGWANSSLNPIIYAF-NADFRKAFSTL 344

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186 KRKENONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOIOMLOR 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 AAEHAQSCRINRLECQHHNTLKTSIKRETKVFKTLSVIMGVFVCCWLPFFILNCIVPFCD 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 Y------TVPGQVWTAFLWLGYINSGLNPFLYAFLNKSPRRAFLIILCCDDERYRR 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 RPPTDHTAGLPCVSDTTFDVFVWFGWTNSSLNPIIYAF-NADFRKAFASLLGCRNFCSRT 371
                    RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 WLFGK-FCETWIAFDIMCSTASILNLCIISVDRYMAI-ASPFRYERROTORVAFIMIGVA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 WVIPTFISFLPIMOGWNNIGIIDLERSINQGIGQDFHAIEKRKFNQNSNSTYCVFMVNKP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 YAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRAGASSESRPQSAUQHSTHRM 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 YAISSSLISFYIPVVIMIGTYTRIYRIAQTQIRRISSLERAVEQAQSHQHPSDCANENSL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT----ETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID-----YTVPGQVWTAFLWL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 KTTFKKETKVLKTLSIIMGVFVFCMLPFFVLNCMVPFCDIGEIGDPLCVSDSTFNIFVWF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 LSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLAFADLLVSVLVMPFGAIELVQDI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 LFLLIVSTLLGNTLVCAAVIKRRHLRSKVTNFFVISLAVSDLFVAVLVMPRKAVSEVAGY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DO 10010021; Cintegral to membrane; IEA.

CO 1001001692; Freedpror activity; IEA.

CO 10010184; Freedpror activity; IEA.

CO 10010184; Freedproin-like receptor protein signalin. .; IEA.

InterProp. IRRO0276; GSCE_Randpan.

FRINE; FR00277; GTCRR00098.

FRINE; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.

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FROEIF; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.

FROEIF; FR00277; GTCRR00098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parly emergence of three dopamine D1 receptor subtypes in vertebrates. Molecular phylogometic, pharmacological, and functional oriteria defining D1A, D1B, and D1C receptors in European eel Anguilla oriteria defining D1A, D1B, and D1C receptors in European eel Anguilla
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Bikaryotea Metaaoa Chordata, Cranista, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
MEDLINE-971600
CRACHARD B. Stgamori K.S., Coudouel S., Vincent J.D., Nizmik H.B.,
CRACHARD B., Stgamori K.S., Coudouel S., Vincent J.D., Nizmik H.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Siol. Chem. 272:2778-27897).
-- SUDGELDIAL MOOFTON: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-- SHILAKAITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL. 1623-271. AACGOGGS.1.
-- THE PROTEIN COUPLED RECEPTORS.
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Local Similarity 37.9%; Pred. No. 5.5e-1.,
Onnervative 59; Mismatches 114; Indels
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
341 LCCDDERYRRPSILGQTVPCSTTTINGSTHVL 372
                                              345 LGC----YRLCPTTNNAI--ETVSINNGAVV 370
                                                                                                                                                                                    448 AA
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                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=7936;
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12;

46; Gaps

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PERYERRATORVAFVMISUTWITLSVLISPIPVOLINWHKAS--DEEVWIN---GISF---- 198

-----GEKSENCDSSLNREYAISSSLISPYIPVAIMIVTYTRIYRIAQIQIRRISSLER 252

P----SILGQTVPCSTTT-----INGSTHVLRDAVEC 378 PVETVNISNELVSYNQDTLPHKEIVTAYVNMIPNVVDC 409

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126 PLVYRNIOMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIE 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             andquilla."; Chem. 272:2778-2787(1897).

J. BAOL Chem. 272:2778-2787(1897).

L. SUBCELLULAR LOCATION INTEGRAL MERBRANE PROTEIN (BY SIMILARITY).

L. SIMILARITY: BELOAK OF FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

BRUIL, UGS201, CLINEGRAI to emebrane; IRA.

CON GOUGOLS, PIREGRAI to emebrane; IRA.

CON GOUGOLS, PIREGRAI TO CALL'HY, IRA.

CON GOUGOLS, PIREGRAI THE RECEPTOR ACTIVITY; IRA.

CON GOUGOLS, PIREGRAI THE RECEPTOR ACTIVITY; IRA.

CON GOUGOLS, PIREGRAI THE RECEPTOR ACTIVITY; IRA.

CON GOUGOLS, PROGRAIN-THE RECEPTOR ACTIVITY; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Early emergence of three dopamine D1 receptor subtypes in
vertebraces Mobilar Divogenetic, pharmacological, and functional
vertebraces mobile and D1, and D1C receptors in European sel Anguilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SSEEGFGSVEKVVLLT---FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLAFA
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Marayota / Metazoa, Chordata, Crantata, Vertebrata; Buteleostomi;
Actinoptecayai, Meoperygii, Teleostei, Angulliformes; Angulliidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.4%; Score 564; DB 13; Length 458; 35.4%; Pred. No. 1.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 141; Conservative 63; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMELrel. 02, Created)
01-FEB-1997 (TrEMELrel. 02, Last sequence update)
1-UN-2003 (TrEMELrel. 24, Last annocation update)
     340
312 GWANSSLNPVIYAP-NADFRKAFSTILGCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97160583; PubMed=9006917;
                                                                                                                                                                                               PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                  Dopamine D1B receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=7936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Branchiostona lanceolatum (Common lancelet) (Amphioxus).
Brikaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae;
Branchiostona.
                                                                                                                                                                                                                                                                                                                Best Local Similarity 38.5
Matches 135, Conservative
                                                            SEQUENCE FROM N.A.
                                       NCBI_TaxID=7740;
                                                                                                                                                                                                                                                                                                       Query Match
       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .00 VAEVAGYWPFG-AFCDVWVAFDIMCSTASILNLCVISVDRYMAI-SRPFRYKRKNTQRMA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTYCVPM/NXPYAITCSVVAFYIPFILMVLAYYRIYVTAKEHAHOIOMLQRAGASSESR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 RSSAACAPDXSLRASIKKETKVLKTLSVIMGVFVCCWLPFFILNCMVPFCSGHPEGPPAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 PPCVSETTFDVFVWFGWANSSLNPVIYAF-NADFQXVFAQLLGCSHFCSRTPV---BTVN 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ALMLGGCWVIPTFISFLPIMQGWN-----NIGIIDLERSLNQGLGQDFHAIEKRKFNQNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 PQSA----DQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFIDYTVPG---- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QVWIAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVP 359
                                                                                                                                                                                                                                                                   .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                      19 KVVLLTFLSTVILMAILGNLLVMVAVC#DRQLRKIKTNYFIVSLAFADLLVSVLVMPFGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                  40 QVVTACLLILLIIWTLIGNVIVCAAIVRSRHLRANMTNVFIVSLAVSDLPVALLVMPWKA 99
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                               43:
                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 477;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.4%; Score 563.5; DB 4; Length 4 Best Local Similarity 34.7%; Pred. No. 28-46; Matches 137; Conservative 69; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                  477 AA; 52960 MW; FFB0B7662D36BAF2 CRC64;
                                                                                  (TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 CSTTTIN-----GSTHVLRDAVECGGG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 ISNELISYNODIVFHKEIAAAYIHMMPNAVTPGNR 423
                                                   477 AA
                                                                         Created)
                                                                       (TrEMBLrel. 22,
                                                  PRELIMINARY;
                                                                                                         Dopamine receptor D5.
                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                        SEOUENCE FROM N.A.
                                                                                                                                                                 NCBI TaxID=9606,
                                                                         01-OCT-2002
                                                                                  01-OCT-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                       Receptor.
                                                                                                                                                                                                                                                                                                                                                    SECUENCE
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Last sequence update) Last annotation update)

(TrEMBLrel. 10, (TrEMBLrel, 24, 01-MAY-1999 (TrEMBLrel. 10, Dopamine D1/beta receptor.

01-MAY-1999 01-JUN-2003

Created) PRT;

391 AA

PRELIMINARY;

911960

RESULT 15 096716 ID 09671 AC 09671 DT 01-MA DT 01-MA DT 01-MA DT 01-MA

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53 IXTNYFIVSLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 CISLDRYYAICCQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 YRDNOSEEALAI -----YSDPCLCIFTASTAYTIVSSLISFYIPLLIMLVPYGIIFKA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEBLE, AUGOSAI, CAAGES, I. .

GO, GO10601; C:hiregral to emebrane; IEA.

GO; GO10601; F:resegral to emebrane; IEA.

GO; GO1060159; F:resegral or activity, IEA.

GO; GO106159; F:resegral coupled receptor activity, IEA.

INC. GO; GO106199; F: Grand coupled receptor protein signalin. .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 VIAFDRFLAITA-PFTYHTRMTERTAGILIATVWGISLVVSFLPIQAGW------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AKEHAHQIQMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Gaps
Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S., Guibert B.,
Wincent J.D., Marint H.B., Vernier P.;
Wincent JD., Marint H.B., Vernier P.;
The amphibosus Dilbeta receptor and the emergence of the vertebrate
                                                                                                                                                                                                                                          adrenerjic system.")
Subaired (ART-100ATO): Lothe EMBL/GenBank/DDBJ databases.
--- STRECELLUDAR 100CHTON: INFESBAL MEMBRANE PROTEIN (BY SIMILARITY)
--- SIMILARITY: BELOGGS TO FUMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 562; DB 5; Length 39
38.5%; Pred. No. 2.3e-46;
ive 57; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42622 MW; 67A5AD944AFA3FBE CRC64;
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